

FIG. 1

FIG. 1A

1 tcttcctaccatctgctccccagagggtgcctgctgtgcacttgggtcctggagccctctccaccggatagattcctcaccttggcccgctttg
101 cccaccctactctgcccagaagtgcagagcctaagccgctccatggccccaaggagattcaggggagaggccccaaacaggaggccacgccagcca
-20 -10
MetGluLeuThrGluLeuLeuValValMetLeuLeuLeuThrAlaArgLeuThrLeuSerSerProAlaProProAlaCysAsp
201 gacaccccgccagaaATGGAGCTGACTGAATTGCTCCTCGTGGTCATGCTTCTCTAACTGCAAGGCTAACGCTGTCCAGCCCGCTCCTCTCTGTTGT
10 20 30 40
LeuArgValLeuSerLysLeuLeuArgAspSerHisValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThrProValLeuLeu
301 ACCTCCGAGTCTCAGTAACTGCTTCGTGACTCCCATGTCCTTCACAGCAGACTGAGCCAGTGCAGAGGTTACCCCTTTGCTTACACTGTCTCTGCT
50 60 70
ProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGlyGlyVal
401 GCCTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAGGCACAGGACATTCTGGGAGCAGTGACCCTTCTGCTGGAGGAGCTG
80 90 100
MetAlaAlaArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeu
501 ATGGCAGCAGCGGGACAACCTGGGACCCACTTGCTCTCATCCCTCTGGGACAGCTTTCTGGACAGGTCCGCTCTCTCTTGGGCCCCGACAGGCTCC
110 120 130 140
GlyThrGlnLeuProProGlnGlyArgThrThrAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysValArgPhe
601 TTGGAACCCAGCTTCTCCACAGGGCAGGACCACAGCTCACAAGGATCCCAATGCCATCTTCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTGCTTT
150 160 170
LeuMetLeuValGlyGlySerThrLeuCysValArgArgAlaProProThrThrAlaValProSerArgThrSerLeuValLeuThrLeuAsnGluLeu
701 CCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTCAGGCGGGCCCCACCCACACAGCTGTCCCCAGCAGAACCTCTCTAGTCTCACACTGAACGAGCTC
180 190 200
ProAsnArgThrSerGlyLeuLeuGluThrAsnPheThrAlaSerAlaArgThrThrGlySerGlyLeuLeuLysTrpGlnGlnGlyPheArgAlaLysIle
801 CCAACAGGACTTCTGGATTGTTGGAGACAACTTCAGTGCCTCAGCCAGAACTACTGGCTCTGGGCTTCTGAAGTGGCAGCAGGGATTACAGAGCCAAGA
210 220 230 240
ProGlyLeuLeuAsnGlnThrSerArgSerLeuAspGlnIleProGlyTyrLeuAsnArgIleHisGluLeuLeuAsnGlyThrArgGlyLeuPhePro
901 TTCCTGGTCTGCTGAACCAAACTCCAGGTCCTGGACCAAAATCCCGGATACCTGAAACAGGATACACGAACTCTTGAATGGAACCTGTGGACTCTTTCC
250 260 270
GlyProSerArgArgThrLeuGlyAlaProAspIleSerSerGlyThrSerAspThrGlySerLeuProProAsnLeuGlnProGlyTyrSerProSer
1001 TGGACCCTCAGCAGGACCTAGGAGCCCGGACATTCTCAGGAACATCAGACACAGGCTCCCTGCCACCCAACCTCCAGCCTGGATATTCTCTCTCC
280 290 300
ProThrHisProProThrGlyGlnTyrThrLeuPheProLeuProProThrLeuProThrProValValGlnLeuHisProLeuLeuProAspProSerAla
1101 CCAACCCATCTCTACTGGACAGTATACGCTCTTCCTCTTCCACCCACTTGCCCAACCCTGTGGTCCAGCTCCACCCCTGCTTCTGACCTTCTG
310 320 330
ProThrProThrProThrSerProLeuLeuAsnThrSerIleThrHisSerGlnAsnLeuSerIleGlnGlyGly
1201 CTCCAAGCCCCACCCCTACCAGCCCTCTTCTAACACATCTACACCCACTCCAGAACTGTCTCAGGAAGGGTAAGgttctcagacactgccgacatc
1301 agcattgtctcatgtacagctcccttccctgcagggcgccctgggagacaactggacaagatttctacttttctcctgaaacccaagccctggtaaaa
1401 gggatcacacaggactgaasaggggaatcatttttctactgtacattataaaccttcagaagctattttttaagctatcagcaatactcatcagagcagcta
1501 gctctttgggtctattttctgcagaaatttgcaactcactgattctctacatgctcttttctgtgataactctgcaaggcctgggctggcctggcagtt
1601 gaacagagggagagactaaccttgagtcagaaaaacagagaaagggtaatttcttctgcttcaattcaaggccttccaagcccccatccctttactat
1701 cattctcagtgaggactctgatcccatattcttaacagatctttactcttgagaatgaataagctttctctcagaaaaaataaaaaaaaaaaaaa

FIG. 1B

FIG. 1A

1 tcttctaccatctgtctccccagagggctgcctgtgtgcaacttgggtcctggagcccttctccaccggatagattcctcacccttggccccgcttgg

101 cccccaccctactctgtccccagaagtgaagagcctaagcgcctccatggccccaggaaggattcaggggagagggccccaaacagggagccacgccagcca

201 gacacccccggccagaaATGGAGCTGACTGAATTGCTCTCCTCGTGGTCATGCTTCTCTAACTGCAAGGCTAACGCTGTCCAGCCCCGGCTCCTCTGCTTGTG

301 ACCTCCGAGTCCCTCAGTAAACTGCTTCGTGACTCCCCATGTCTTCACAGCAGACTGAGCCAGTGCCCGAGAGGTTACACCTTTGCTTGCCTACACCTGTCTCTGCT

401 GCCTGCTGTGGACTTTAGCTTGGGAGAAATGGAAACCCAGATGGAGGAGACCAAGGCACAGGACATCTGGGAGCAGTGACCTTCTGCTGGAGGGAGTG

501 ATGGCAGCACGGGGACAACACTGGGACCCACTTGCTCTCATCCCTCCTGGGCAGCTTCTGGACAGGTCCGTCTCCTTTGGGGCCCTGCAGAGCCTCC

601 TTGGAACCCAGCTTCTCCTCCACAGGGCAGGACCACAGCTCACAAAGGATCCCAATGCCATCTTCTCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTGCGTTT

701 CCTGATGCTTGTAGGAGGGTCCACCCCTCTGCGTCAGGCGGGCCCCACCCACCACACAGCTGTCCCCAGCAGAACCTCTCTAGTCTCCTCAGACTGAACGAGCTC

801 CCAAACAGGACTTCTGGATTCTTGGAGACAAACTTCACTGCCTCAGCCAGAACTACTGGCTCTGGGCTTCTGAAGTGGCAGCAGGGATTTCAGAGCCAAGA

MetGluLeuThrGluLeuLeuLeuValMetLeuLeuLeuThrAlaArgLeuLeuThrLeuSerSerProAlaProProAlaCysAsp

LeuArgValLeuSerLysLeuLeuArgAspSerHisValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThrProValLeuLeu

ProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuGluGlyVal

MetAlaAlaArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeuGlyAlaLeuGlnSerLeuLeu

GlyThrGlnLeuProProGlnGlyArgThrThrAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysValArgPhe

LeuMetLeuValGlyGlySerThrLeuCysValArgArgAlaProProThrThrAlaValProSerArgThrSerLeuValLeuThrLeuAsnGluLeu

ProAsnArgThrSerGlyLeuLeuGluThrAsnPheThrAlaSerAlaArgThrThrGlySerGlyLeuLeuLysTrpGlnGlnGlyPheArgAlaLysIle

FIG. 1B

	210	220	230	240
901	ProGlyLeuLeuAsnGlnThrSerArgSerLeuAspGlnIleProGlyTyrLeuAsnArgIleHisGluLeuLeuAsnGlyThrArgGlyLeuPhePro			
	TTCTGGTCTGCTGAACCAACCTCCAGGTCCCTGGACCAATCCCGGATACCTGAACAGGATACAGAACTCTTGAATGGAACTCGTGGACTCTTTCC			
	250	260	270	
1001	GlyProSerArgArgThrLeuGlyAlaProAspIleSerSerGlyThrSerAspThrGlySerLeuProProAsnLeuGlnProGlyTyrSerProSer			
	TGGACCCCTCAGCAGGACCCCTAGGAGCCCCGGACATTTCCTCAGGAACATCAGACACAGGCTCCCTGCCACCCCAACCTCCAGCCTGGATATTCTCCTTCC			
	280	290	300	
1101	ProThrHisProProThrGlyGlnTyrThrLeuPheProLeuProProThrProThrLeuProThrProValValGlnLeuHisProLeuLeuProAspProSerAla			
	CCAAACCCATCCTCTACTGGACAGTATACGCTCTTCCCTCTTCCACCCACCTTGCCCCACCCCTGTGGTCCAGCTCCACCCCTGCTTCTCCTGACCCCTTCTG			
	310	320	330	
1201	ProThrProThrProThrSerProLeuLeuAsnThrSerTyrThrHisSerGlnAsnLeuSerGlnGluGly			
	CTCCAACGCCACCCCTACCAGCCCTCTTCTAAACACATCCTACACCCACTCCAGAAATCTGTCTCAGGAAGGTAAGgttctcagacactgccgacatc			
1301	agcattgtctcatgacagctcccttccctgcaggggccctgggagacaaactggacaagatttccctactttctcctgaaacccaaagccctggtaaaa			
1401	gggatacacaggactgaaaaggggaatcattttcactgtacattataaaccttcagaagctattttttaagctatcagcaatactcatcagagcagcta			
1501	gctctttggtctattttctgcagaaaatttgcaactcactgattctctacatgctctttttctgtgataaactctgcaaaaggcctgggctggcctggcagtt			
1601	gaacagaggagagactaaccttgagtcagaaaaacagagaaaagggtaatctccttgccttcaaatcaaggccttccaacgcccccatccccctttactat			
1701	cattctcagtgaggactctgatcccatattcttaacagatctttactcttgagaaatgaataagctttctctcagaaaaaaataaaaaaa			

FIG. 2

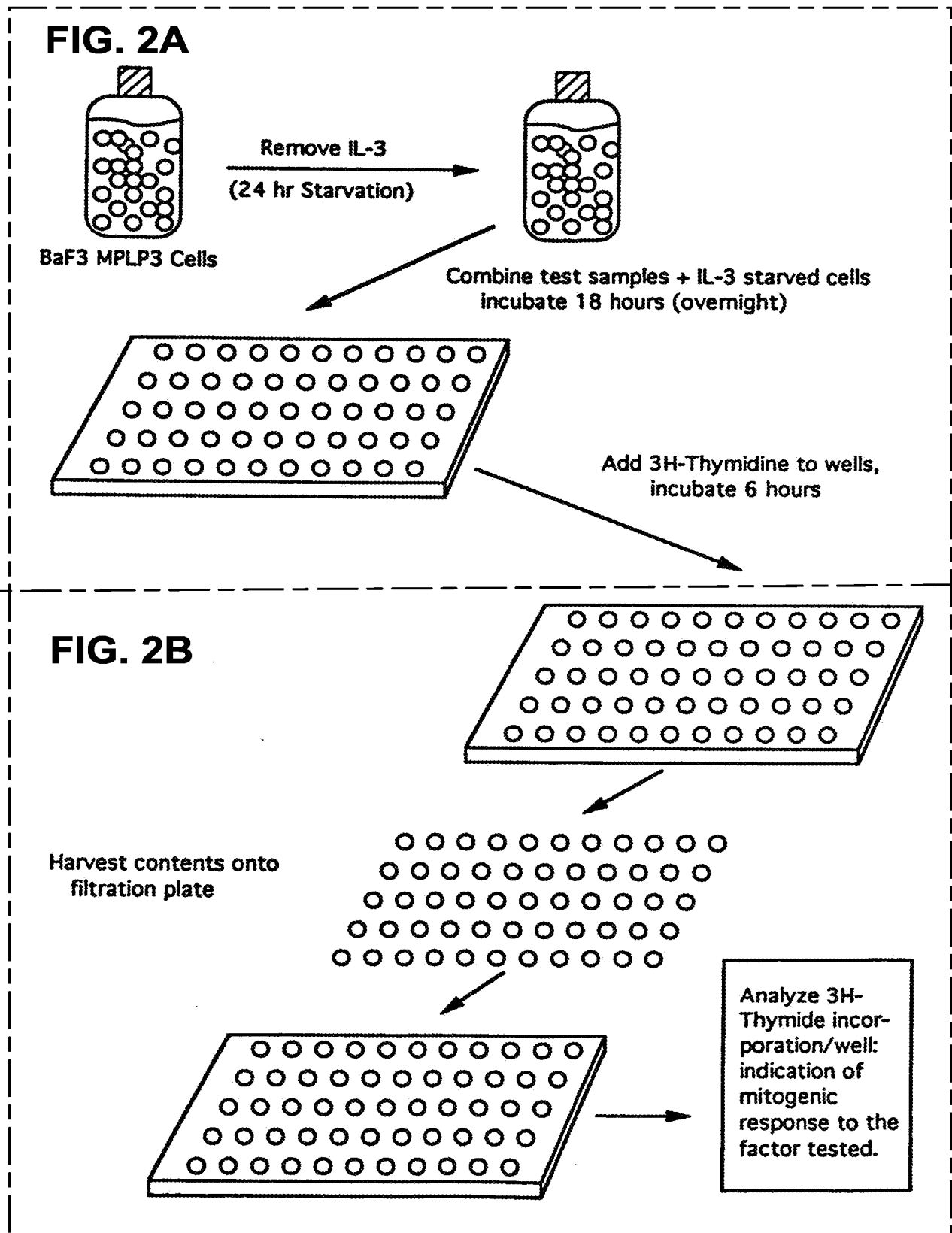
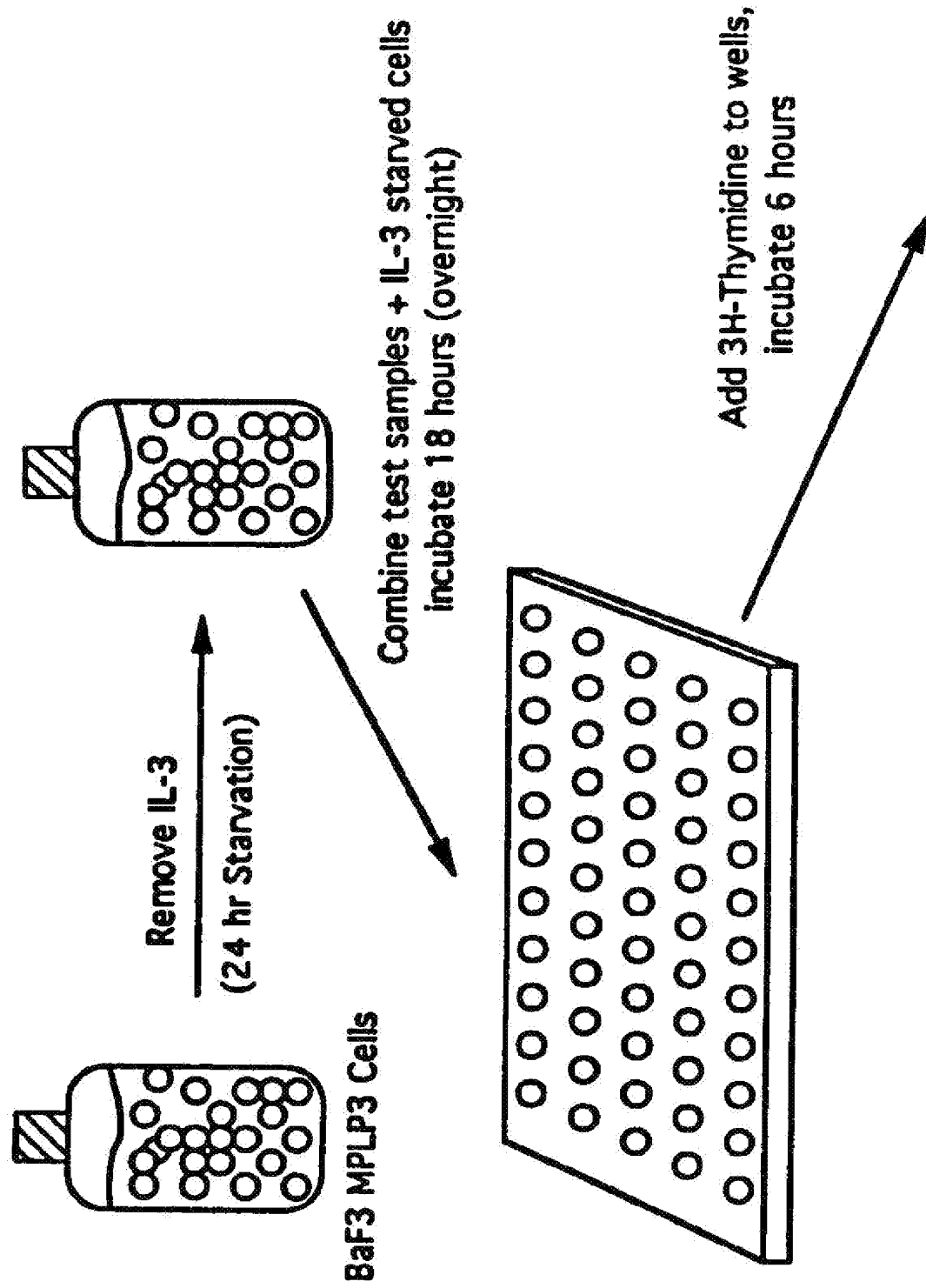
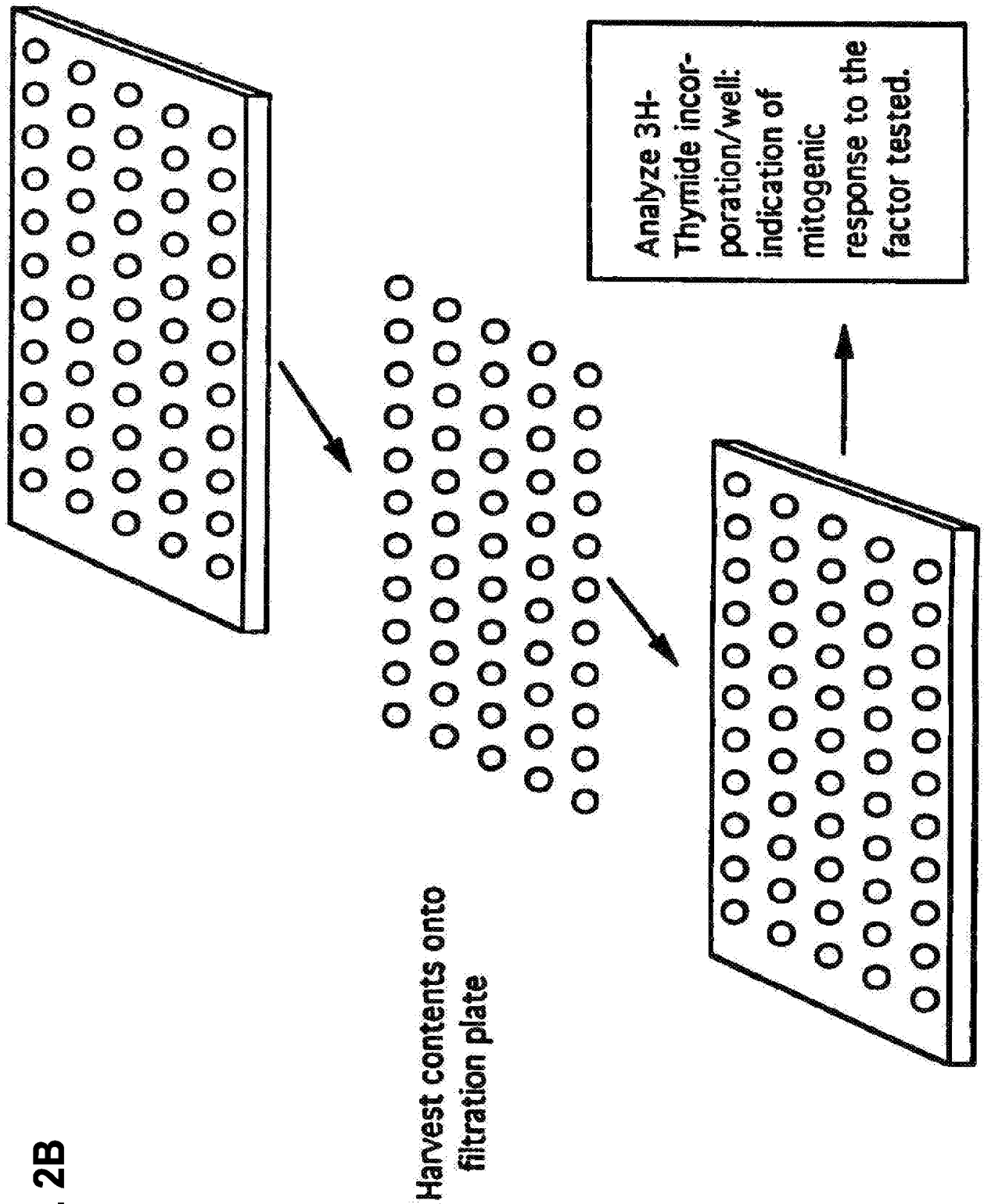


FIG. 2A





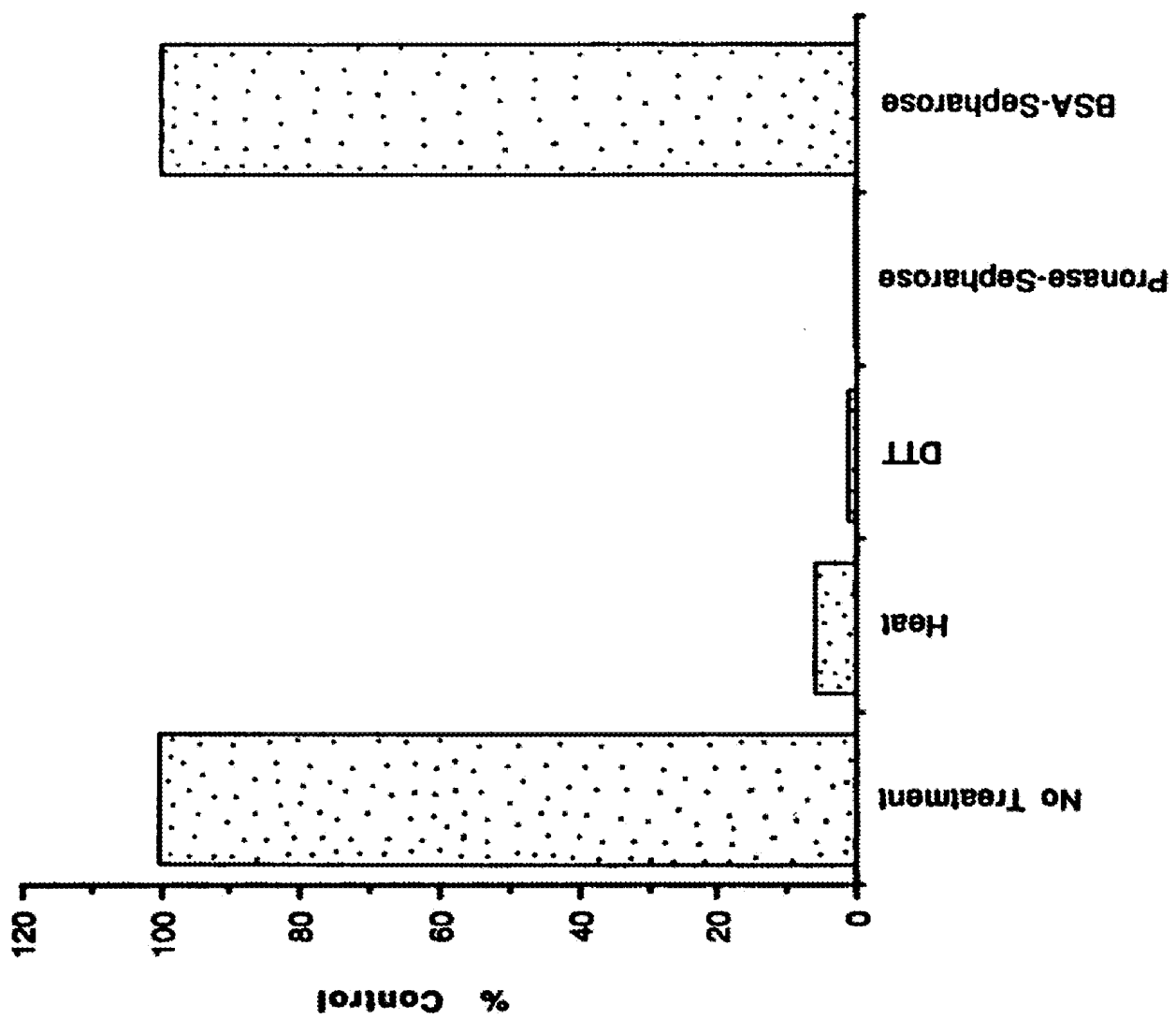


FIG. 3

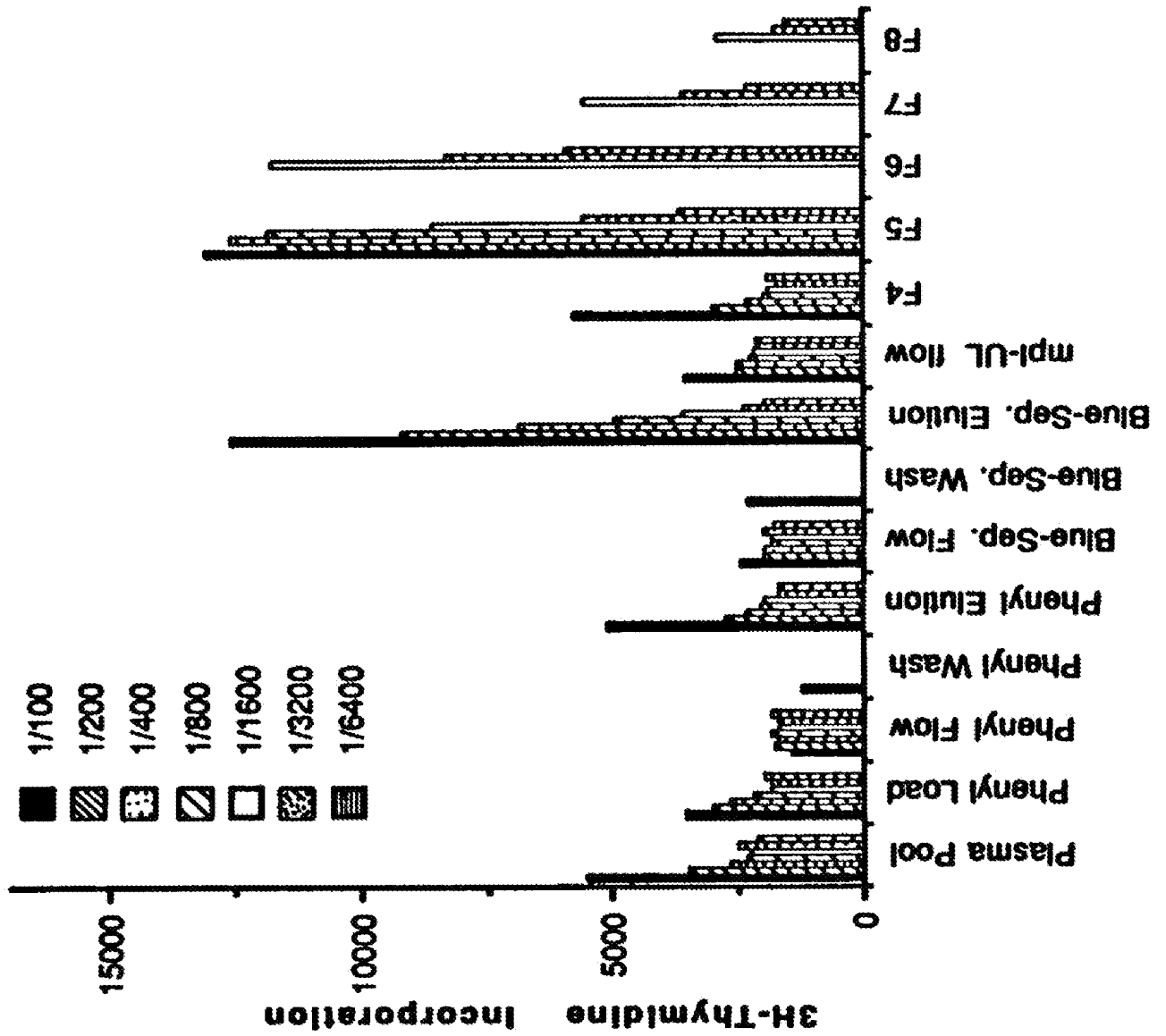


FIG. 4

FIG. 5

MW $\times 10^{-3}$

200.0—

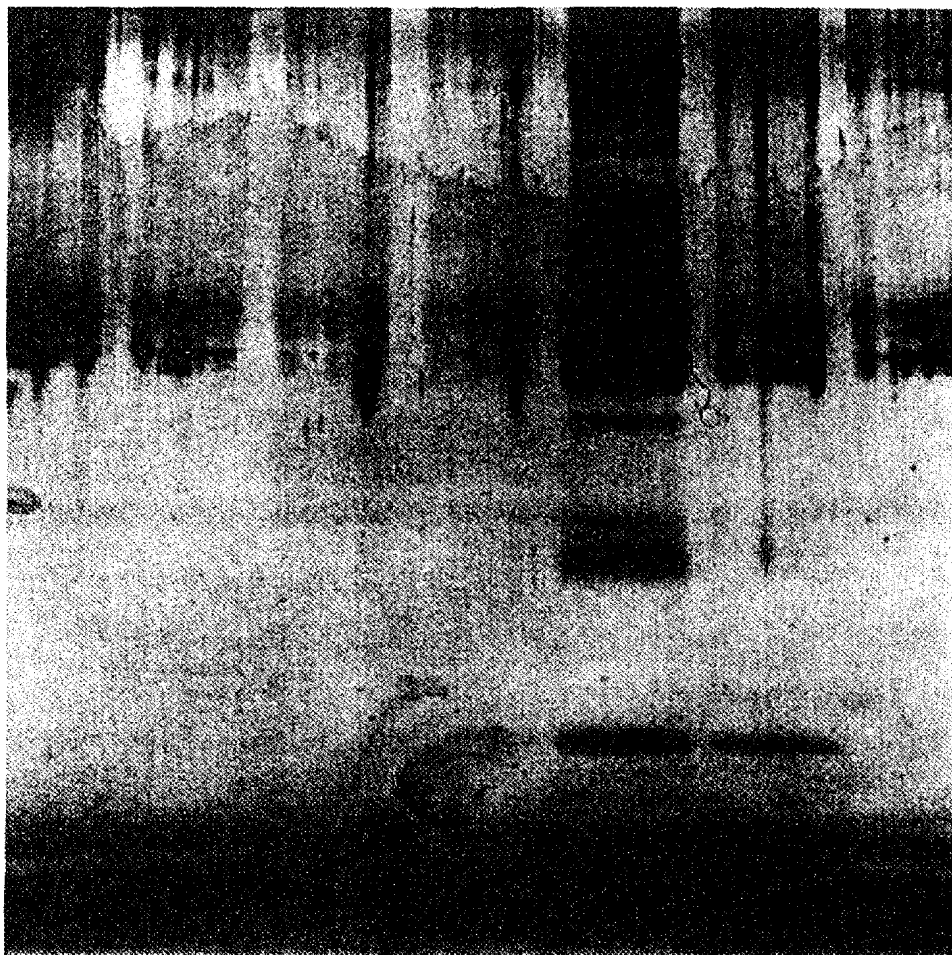
66.3—

36.5—

31.0—

21.5—

14.4—



2

3

4

5

6

7

8

FRACTION NUMBER

FIG.6

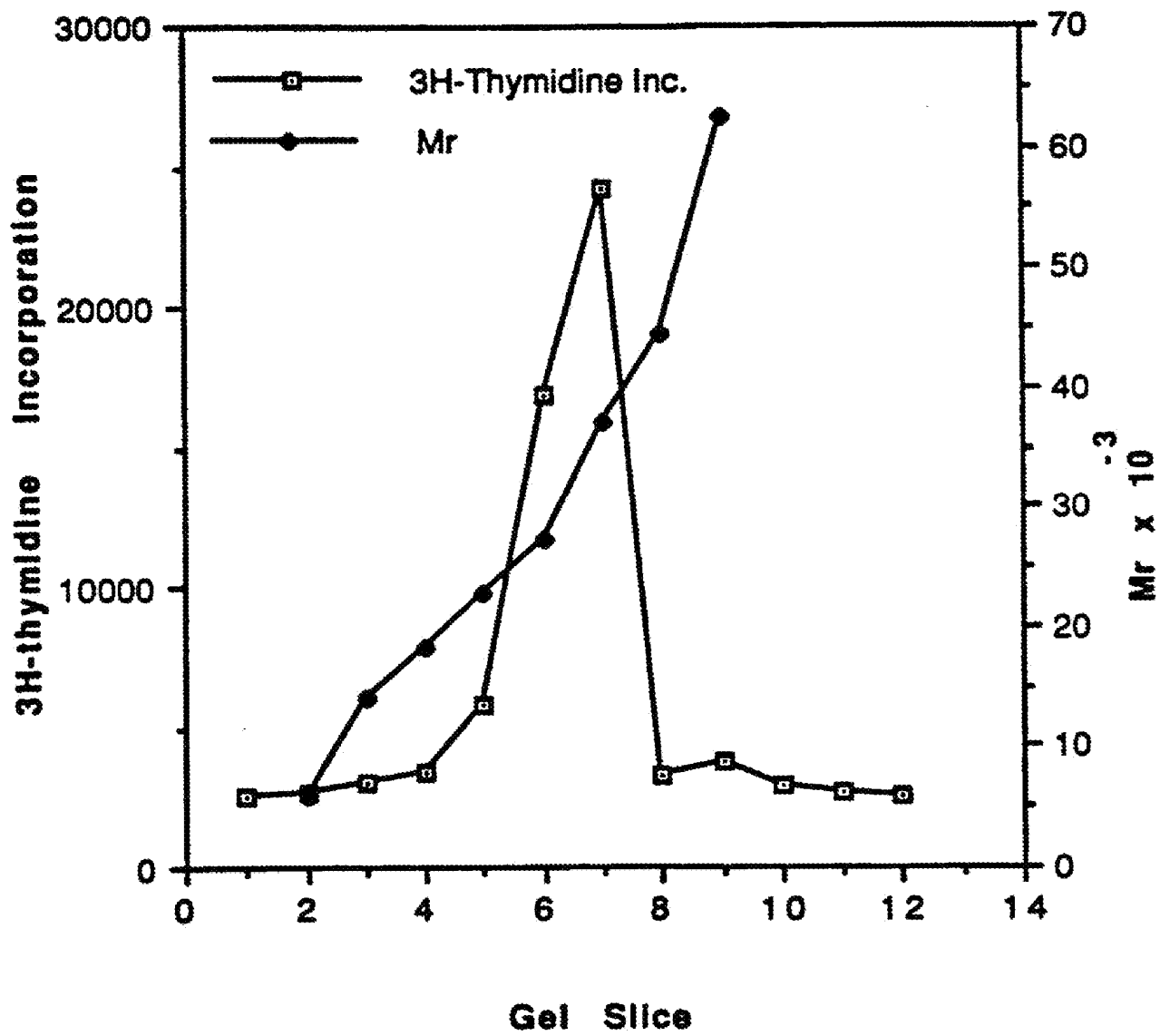
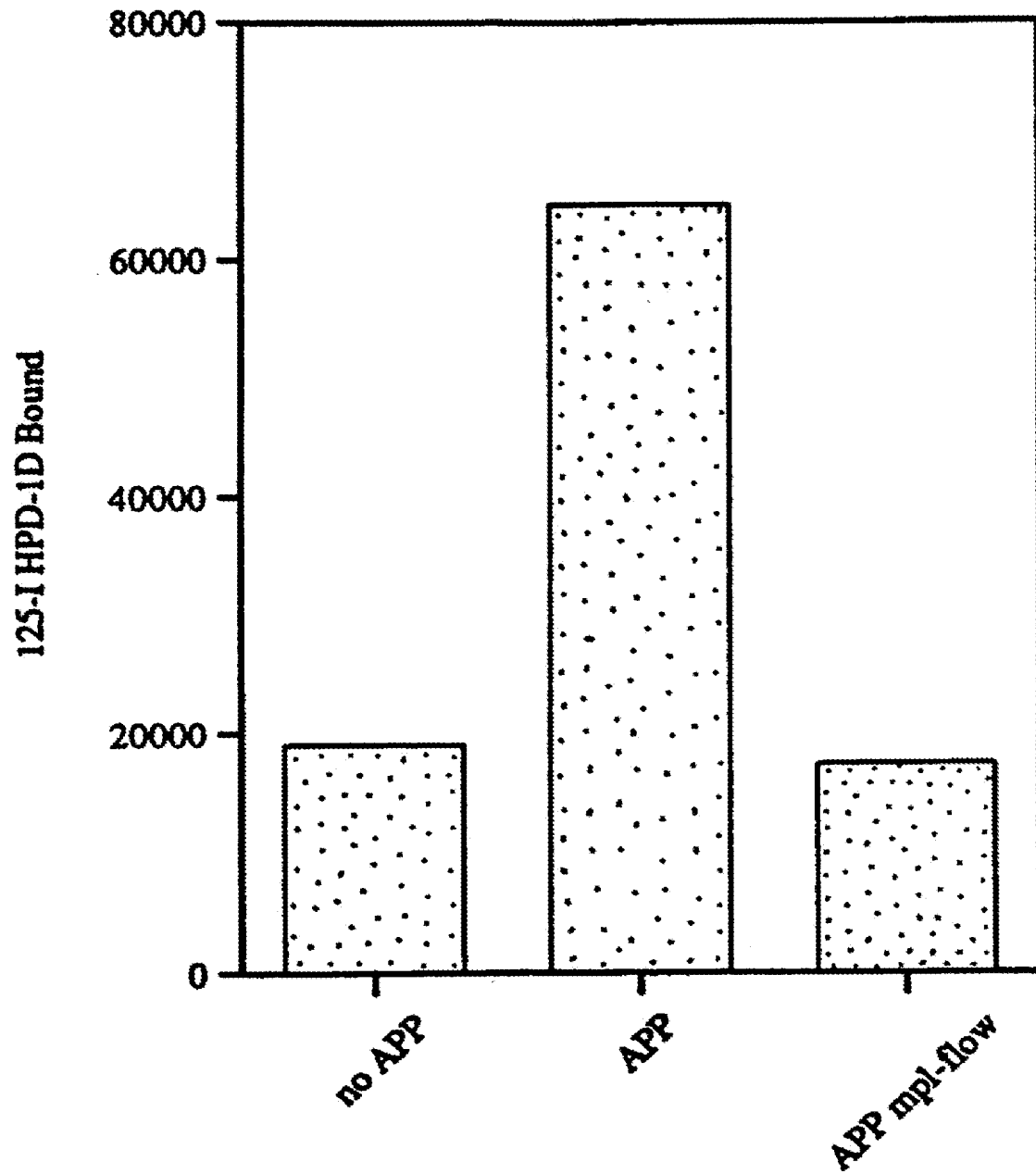


FIG. 7



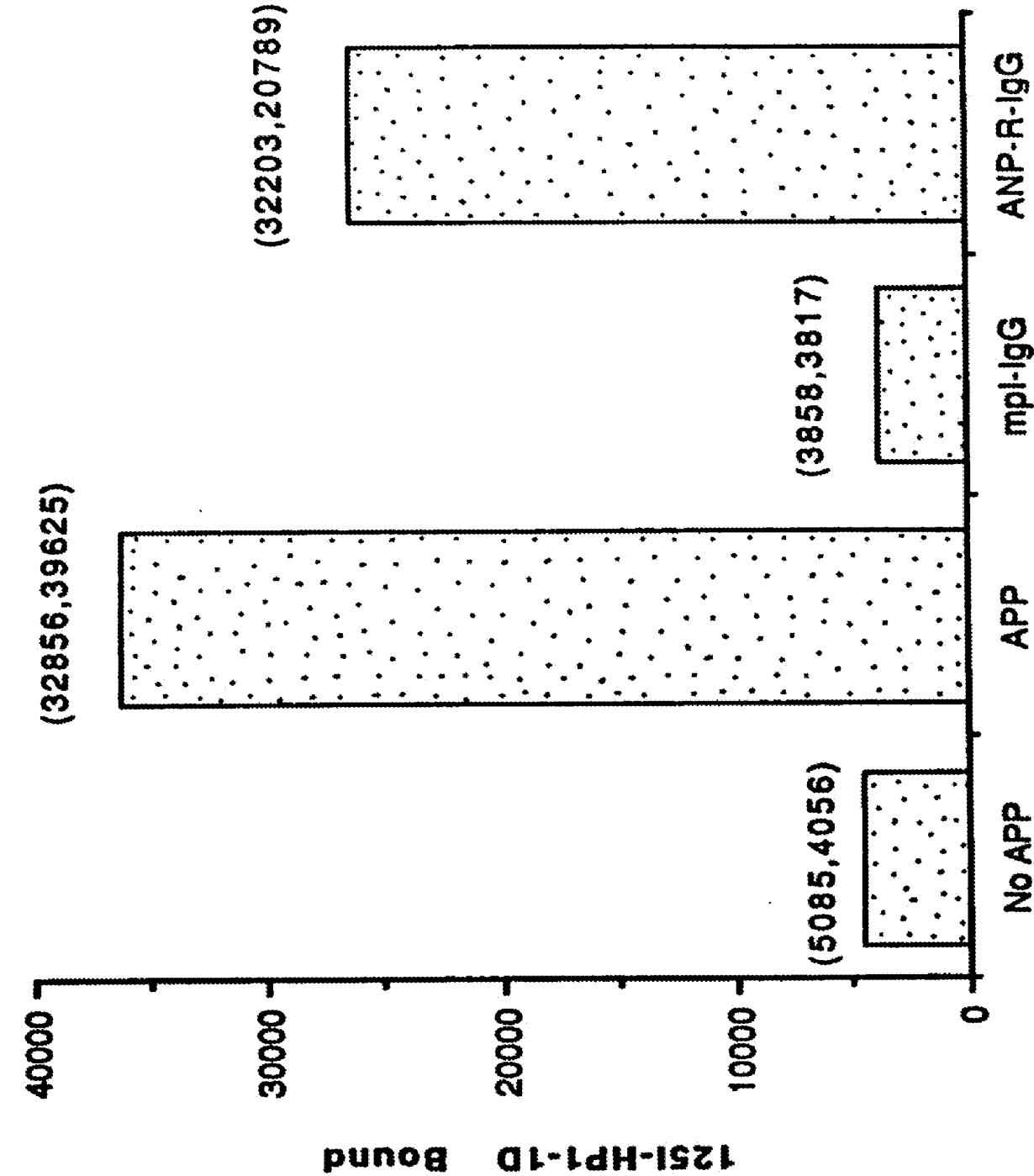


FIG. 9

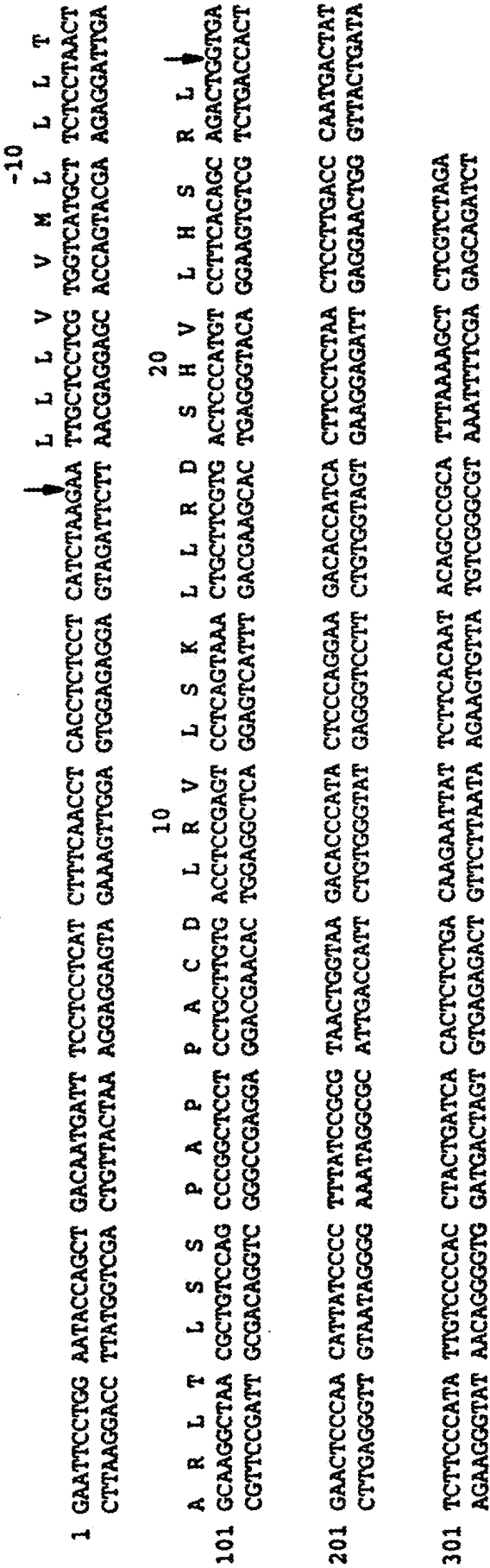


FIG. 11

FIG.11A

hML	1	S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T P V L L P A V D F S L G E
hML2	1	S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T P V L L P A V D F S L G E
hML3	1	S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T P V L L P A V D F S L G E
hML4	1	S P A P P A C D L R V L S K L L R D S H V L H S R L S Q C P E V H P L P T P V L L P A V D F S L G E

hML	51	W K T Q M E E T K A Q D I L G A V T L L L E G V M A A R G Q L G P T C L S S L L G Q L S G Q V R L L
hML2	51	W K T Q M E E T K A Q D I L G A V T L L L E G V M A A R G Q L G P T C L S S L L G Q L S G Q V R L L
hML3	51	W K T Q M E E T K A Q D I L G A V T L L L E G V M A A R G Q L G P T C L S S L L G Q L S G Q V R L L
hML4	51	W K T Q M E E T K A Q D I L G A V T L L L E G V M A A R G Q L G P T C L S S L L G Q L S G Q V R L L

hML	101	L G A L Q S L L G T Q L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S T L
hML2	101	L G A L Q S L L G T Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S T L
hML3	101	L G A L Q S L L G T Q L P P Q G R T T A H K D P N A I F L S F Q H L L R G K . D F W . I V G D K L H
hML4	101	L G A L Q S L L G T Q G R T T A H K D P N A I F L S F Q H L L R G K . D F W . I V G D K L H

hML	151	C V R R A P P T T A V P S R T S L V L T L N E L P N R T S G L L E T N F T A S A R T T G S G L L K W
hML2	147	C V R R A P P T T A V P S R T S L V L T L N E L P N R T S G L L E T N F T A S A R T T G S G L L K W
hML3	149	C L S Q N Y W L W A S E V A A G I Q S Q D S W S A E P N L Q . .
hML4	145	C L S Q N Y W L W A S E V A A G I Q S Q D S W S A E P N L Q . .

hML	201	Q Q G F R A K I P G L L N Q T S R S L D Q I P G Y L N R I H E L L N G T R G L F P G P S R R T L G A
hML2	197	Q Q G F R A K I P G L L N Q T S R S L D Q I P G Y L N R I H E L L N G T R G L F P G P S R R T L G A
hML3	179	V P G P N P R I P . . . E Q D T R T L E W N S W T L S W T L T Q D P R S P G H F L R N I R H R L P A
hML4	175	V P G P N P R I P . . . E Q D T R T L E W N S W T L S W T L T Q D P R S P G H F L R N I R H R L P A

hML	251	P D I S S G T S D T G S L P P N L Q P G Y S P S P T H P P T G Q Y T L F P L P P T L P T P V V Q L H
hML2	247	P D I S S G T S D T G S L P P N L Q P G Y S P S P T H P P T G Q Y T L F P L P P T L P T P V V Q L H
hML3	226	T Q P P A W I F S F P N P S S Y W T V Y A L P S S
hML4	222	T Q P P A W I F S F P N P S S Y W T V Y A L P S S

hML	301	P L L P D P S A P T P T P T S P L L N T S Y T H S Q N L S Q E G
hML2	297	P L L P D P S A P T P T P T S P L L N T S Y T H S Q N L S Q E G
hML3	251	T H L A H P C G P A P P P A S
hML4	247	T H L A H P C G P A P P P A S

FIG.11B

FIG. 11A

hML	1	SPAPPACDLRVLSKLLRDSHVLSHRLSQCPEVHPLPTPVLLPAVDFSLGE
hML2	1	SPAPPACDLRVLSKLLRDSHVLSHRLSQCPEVHPLPTPVLLPAVDFSLGE
hML3	1	SPAPPACDLRVLSKLLRDSHVLSHRLSQCPEVHPLPTPVLLPAVDFSLGE
hML4	1	SPAPPACDLRVLSKLLRDSHVLSHRLSQCPEVHPLPTPVLLPAVDFSLGE
hML	51	WK TQMEETKAQDILGAVTLLLEGVMAARGQLGPTCLSSLLGQLSGQVRLL
hML2	51	WK TQMEETKAQDILGAVTLLLEGVMAARGQLGPTCLSSLLGQLSGQVRLL
hML3	51	WK TQMEETKAQDILGAVTLLLEGVMAARGQLGPTCLSSLLGQLSGQVRLL
hML4	51	WK TQMEETKAQDILGAVTLLLEGVMAARGQLGPTCLSSLLGQLSGQVRLL
hML	101	L G A L Q S L L G T Q L P P Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S T L
hML2	101	L G A L Q S L L G T . . . Q G R T T A H K D P N A I F L S F Q H L L R G K V R F L M L V G G S T L
hML3	101	L G A L Q S L L G T Q L P P Q G R T T A H K D P N A I F L S F Q H L L R G K . D F W . I V G D K L H
hML4	101	L G A L Q S L L G T . . . Q G R T T A H K D P N A I F L S F Q H L L R G K . D F W . I V G D K L H
hML	151	C V R R A P P T T A V P S R T S L V L T L N E L P N R T S G L L E T N F T A S A R T T G S G L L K W
hML2	147	C V R R A P P T T A V P S R T S L V L T L N E L P N R T S G L L E T N F T A S A R T T G S G L L K W
hML3	149	C L S Q N Y W L W A S E V A A G I Q S Q D S W S A E P N L Q . . .
hML4	145	C L S Q N Y W L W A S E V A A G I Q S Q D S W S A E P N L Q . . .

FIG. 11B

hML	201	Q Q G F R A K I P G L L N Q T S R S L D Q I P G Y L N R I H E L L N G T R G L F P G P S R R T L G A
hML2	197	Q Q G F R A K I P G L L N Q T S R S L D Q I P G Y L N R I H E L L N G T R G L F P G P S R R T L G A
hML3	179	V P G P N P R I P . . . E Q D T R T L E W N S W T L S W T L T Q D P R S P G H F L R N I R H R L P A
hML4	175	V P G P N P R I P . . . E Q D T R T L E W N S W T L S W T L T Q D P R S P G H F L R N I R H R L P A
hML	251	P D I S S G T S D T G S L P P N L Q P G Y S P S P T H P P T G Q Y T L F P L P P T L P T P V V Q L H
hML2	247	P D I S S G T S D T G S L P P N L Q P G Y S P S P T H P P T G Q Y T L F P L P P T L P T P V V Q L H
hML3	226	T Q P P A W I F S F P N P S S Y W T V Y A L P S S
hML4	222	T Q P P A W I F S F P N P S S Y W T V Y A L P S S
hML	301	P L L P D P S A P T P T S P L L N T S Y T H S Q N L S Q E G
hML2	297	P L L P D P S A P T P T S P L L N T S Y T H S Q N L S Q E G
hML3	251	T H L A H P C G P A P P P A S
hML4	247	T H L A H P C G P A P P P A S

FIG. 12A

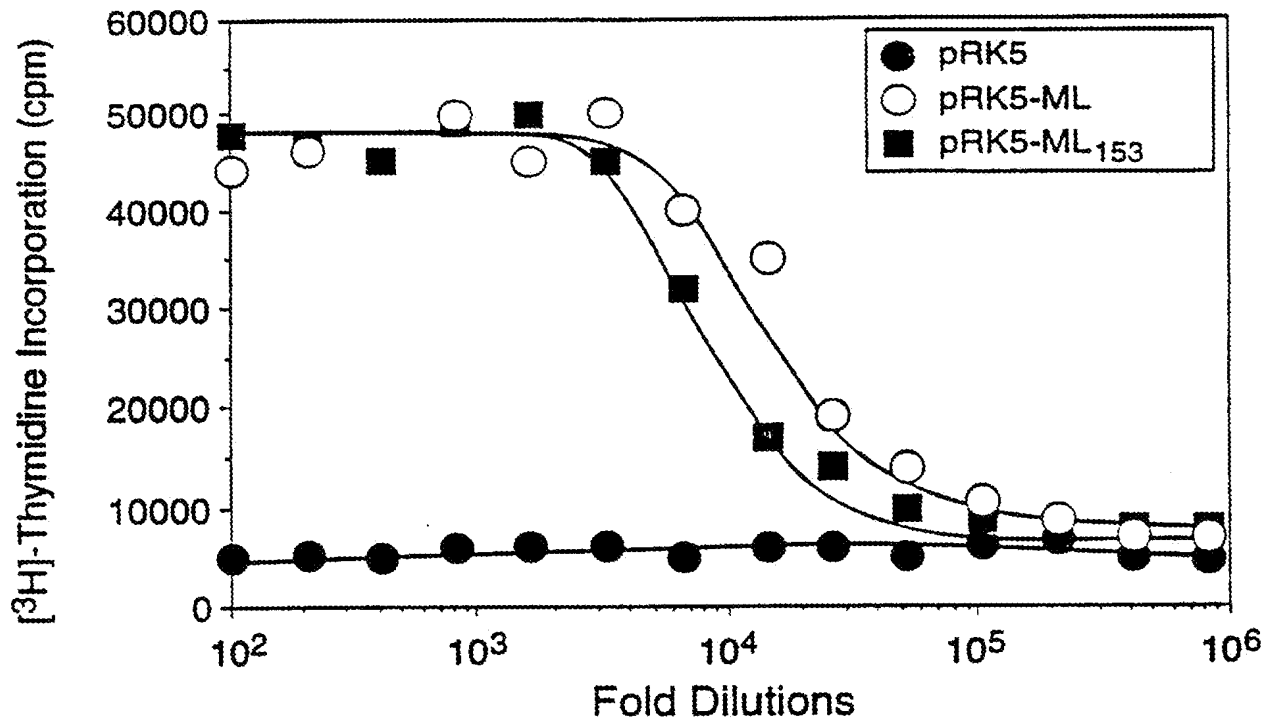


FIG. 12B

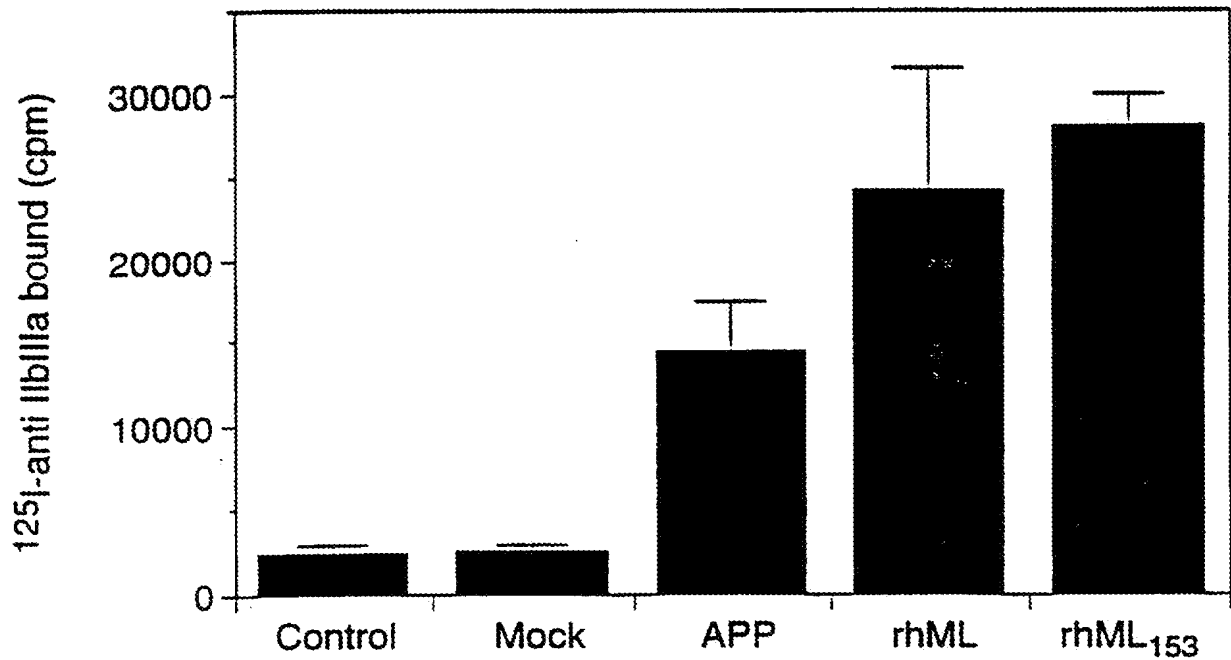


FIG. 12D

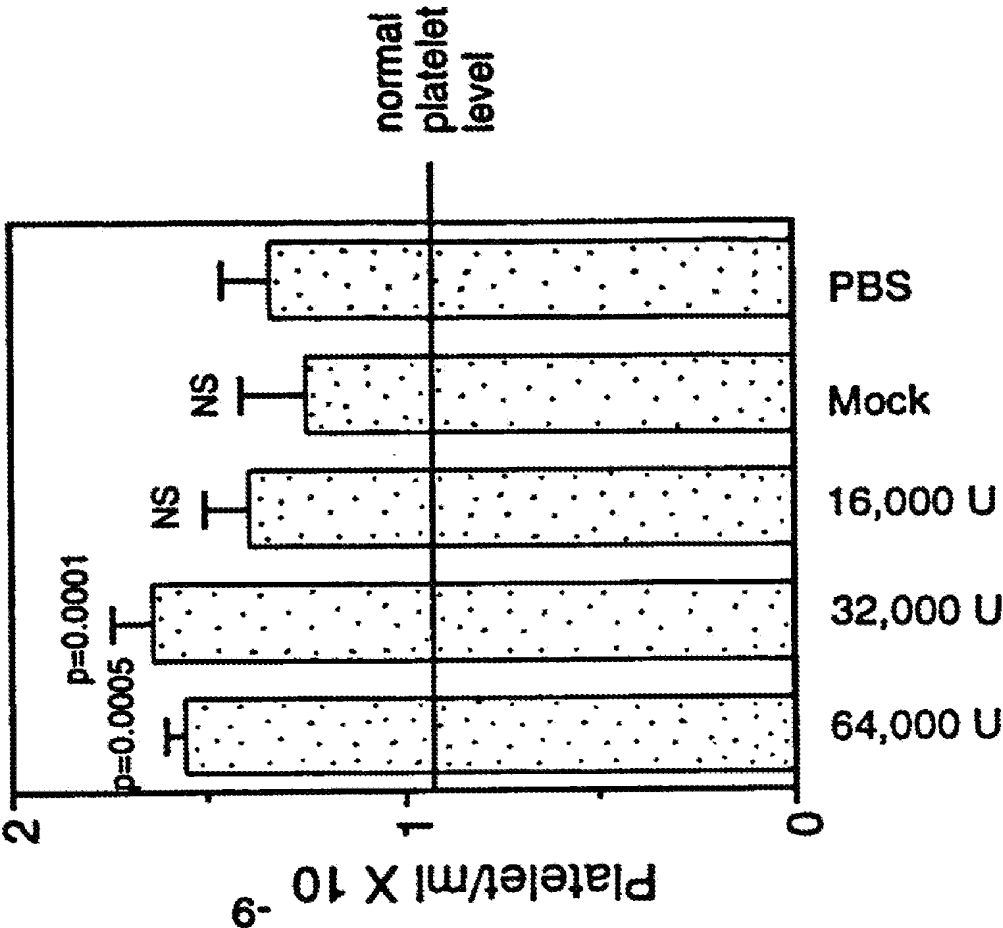
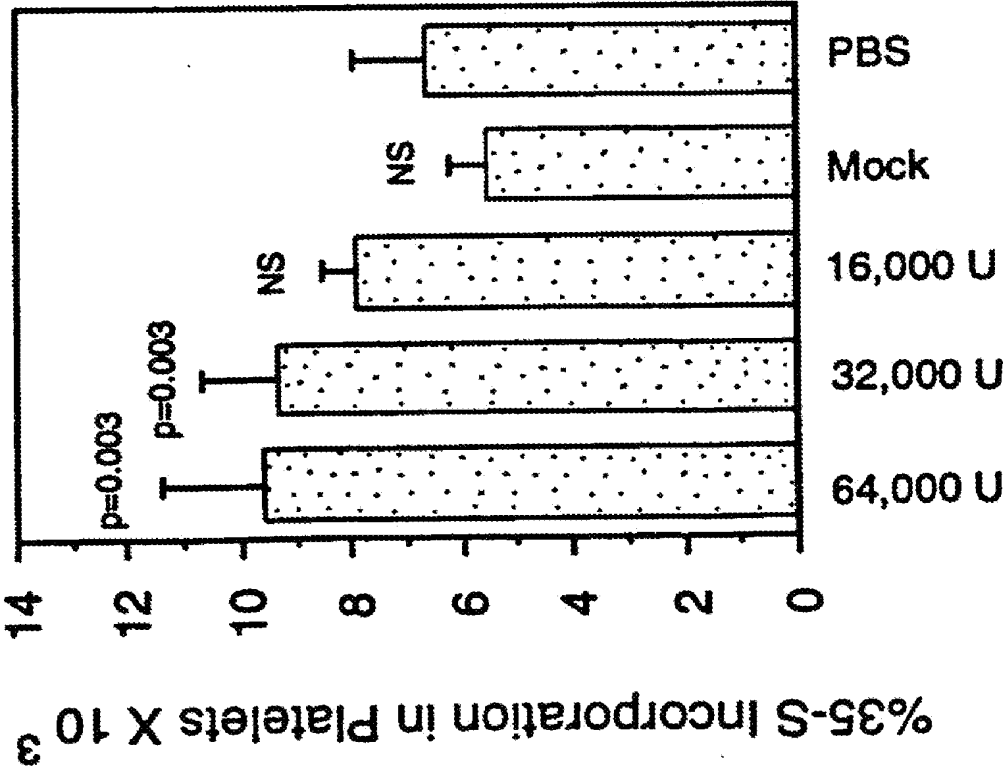


FIG. 12C



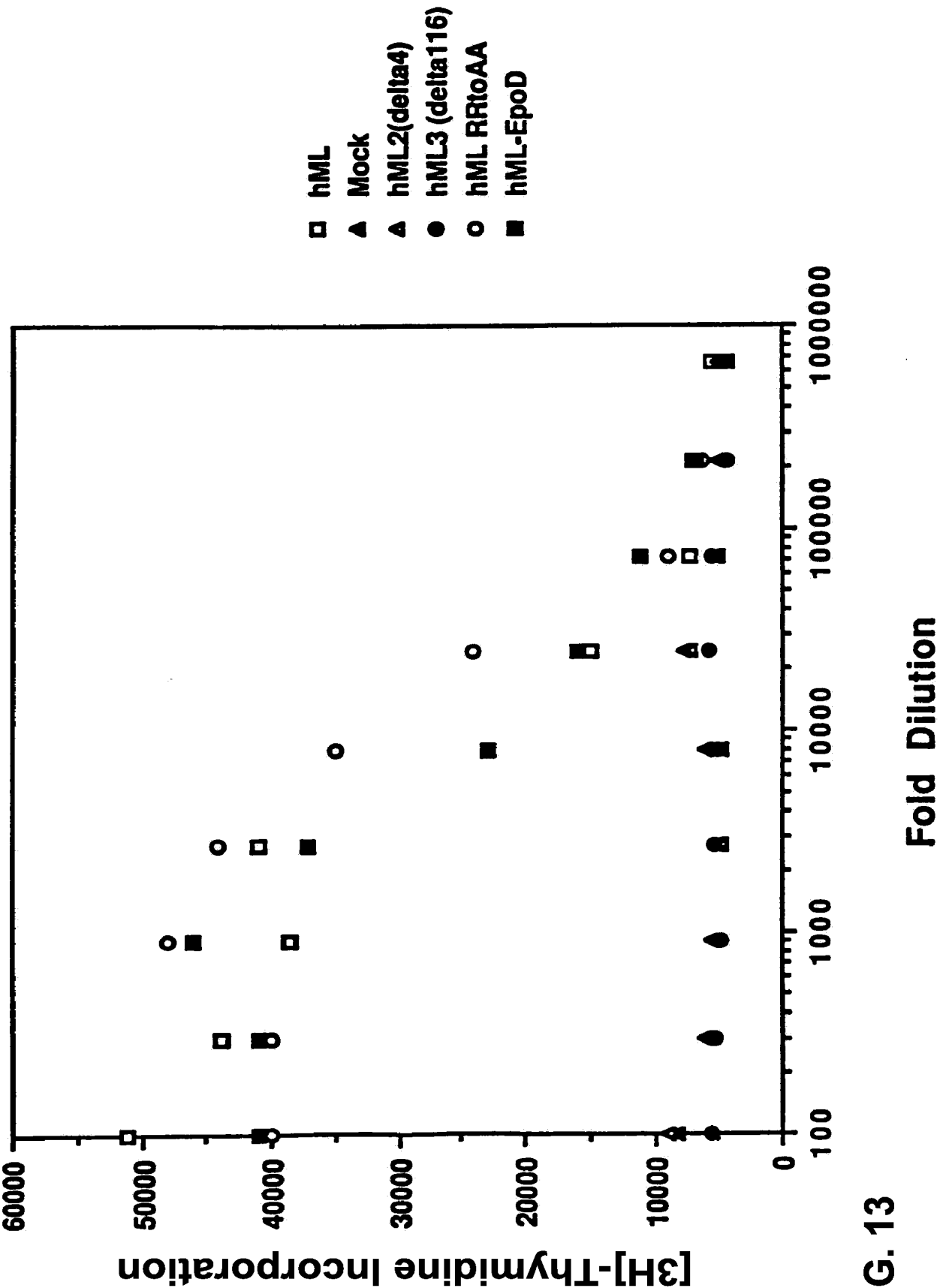


FIG. 13

FIG. 14

FIG.14A

1 GAGTCTCTTGG CCGACCTCTC TCCACGCCGA CTCTGCCGAA AGAAGCAGAG AGCTCTACGC CCGCTCCATG CCGCCAGCGA AGATTTCAGGG GAGAGGCCCC
 ↓
 -10
 Met GluLeuThra splLeuLeu uAlaAlaMet LeuLeuAlaV alAlaArgLe uThrLeuSer
 101 ATACAGCGAG CGACTTCAGT TAGACACCTT GGCACAGATG GAGCTGACTG ATTCTCTCTT GCGCGCATG CTTTCTTCAG TCCCAAGACT AACTCTCTCC
 20
 SerProVala laProAlaCy sAspProArg LeuLeuAsnL yLeuLeuAr gAspSerHis LeuLeuHis eArgLeuSe rGlnCysPro AspValAspPro
 201 AGCCCCGTAG CTCTCTGCTG TGACCCGAGA CTCTTAATAA AACTCTGCTG TGACTCTCCG TCACTCTCAC CTCTTTCACA CCGACTCAG TCGTCTCTCC GAGCTCGACC
 30
 LeuSeril eProValLeu LeuProAlaV alAspPhe sLeuGlyGlu TrpLysThrG InThrGluG l nSerLysAla GlnAspIleL euGlyAlaVal
 301 CTTTCTCTAT CCGCTCTCTG CTCTCTCTCT CTCTCTCTCT TCGACTTTAG CTTCTGAGAA TCGAAATCCG AGACCGAACA GAGGACATTC TAGCGGCAGT
 40
 70
 SerLeuLeu LeuGluGlyV alMetAlaAl aArgGlyGln LeuGluProS erCysLeuSe rSerLeuLeu GlyGlnLeuS eGlyGlnVa lArgLeuLeu
 401 GTCCCTTCTA CTGAGCGAG TGAATGCAGC ACGAGGACAG TTGCAACCTT CTTGCTCTCT ATCTCTCTCT GACACGCTT CTGCGCAGGT TCGCTCTCTC
 80
 LeuGlyAlaL euGlnGlyLe uLeuGlyThr GlnGlyArgT hrThrAlaHi sLysAspPro AsnAlaLeuP heLeuSerLe uGlnGlnLeu LeuArgGlyLys
 501 TTGGGGGCC CCGACGGCTT CCTAGCAACC CAGCGCAGGA CCGACCTTCA CAGGACCCC AATGCCCTCT TCTTCAGCTT CCGACCACTG CTTCCGGGAA
 110
 ValArgPhe ProAsnArgT hrSerGlyLe uLeuGluThr sValArgArg ThrLeuProT hrThrAlaVa lProSerSer ThrSerGlnL euLeuThrLeu
 601 AGGTCCCTT CTCTCTCT GTAGAAGTC CCACTCTCTG TCTCAGAGG ACCCTGCCA CCGACGCTCT CCGAACAGT ACTTCTCAAC TCTCTCACT

FIG.14B

170
 AsnLysPhe ProAsnArgT hrSerGlyLe uLeuGluThr sValArgArg ThrLeuProT hrThrAlaVa lProSerSer ThrSerGlnL euLeuThrLeu
 701 AACACAGTTC CGAAGAGGA CTCTCTGATT CTTCAGAGC AGCTCTCTCTG TCTCAGAGG AACTCTCTCTG TCAAGGCCAG AACTCTCTCTG CTTGACACTC TCGACAGGCT TCGAGGATTC
 180
 ArgValLysI leThrProGl yGlnLeuAsn GlnThrSerA rgSerProVa lGlnIleSer GlyThrLeuA snArgThrHi sGlyProVal AsnGlyThrHis
 801 AGAGTCAAGA TTACTCTCTG TCACTTAAT CAACCTTCCA GGTCCCATCT CCAATCTCT CCAATCTCTA AGCACTTCA CCGACCTCTG AATGGAACTC
 210
 GlyLeuPh eAlaGlyThr SerLeuGlnT hrLeuGluAl aSerAspIle SerProGlyA laPheAsnLy sGlySerLeu AlaPheAsnL euGlnGlyGly
 901 ATGGCTCTT TCGTGGAACT TCACTTCAGA CCGTGAAGC CTGAGACATC TCGCCCGAG CTTTTCAGAA AGGCTCTCTG GCATTTCACC TCCAGGCTG
 240
 LeuProPro SerProSerL euAlaProAs pGlyHisThr pPheProP roSerProAl aLeuProThr ThrHisGlys eProProGl nLeuHisPro
 1001 ACTTCTCTCT TCTCCAGCC TCTCTCTCTG TCGACACACA CCGTCTCTCT CTTACCTCTG CTTGCCAC ACCCATGAT CTCCACCCCA CTTCCACCCC
 270
 LeuPheProA spProSerTh rThrMetPro AsnSerThrA laProHisP roValThrMet TyrProHisP roArgAsnLe uSerGlnGlu Thr
 1101 CTGTTTCTCT ACCCTTCCAC CACCATCCCT AACTCTTACCG CCGCTCTATC AGTCACAAAG TACCTCTCAT CCGAGGATTT GTTCTCAGAA ACATAGCCCG
 310
 1201 GCGACTGCCC CAGTGAAGCT CTCAGACTTC TCTCGGGAG AGCTTCCGCC AGAGGAGCTG AGAGGAGCT GCATCTCTCT CAGATCTTCT CTTTTCACCT
 330
 1301 AAAAGGCTCT GCGGAAGCGA TACACAGCAC TCGAGATTTT AAAATTTTAG CAGCTATTTT TTTTAACTT ATCAGCAATA TTCAATCAGAG CAGCTAGCGA
 1401 TCTTCTGCTT ATTTTCCGTA TAAATTTGAA AATCACTAAT TCT

FIG. 14A

```

1  GAGTCTCTGG CCGACCTCTC TCCACCCGA CTCTGCCGA AGAGCACAG AGCTCAAGC GCGCTCCATG GCGCCAGGAA AGATTCAAGG GAGAGGCCCC
    -20
101 ATACAGGGAG CCACTTCAGT TAGACACCTT GGCACAGATG GAGCTCACTG ATTGCTCTCT Met GluLeuThra sPLeuLeuLe uAlaAlaMet LeuLeuAlaV alAlaArgLe uThrLeuSer
    -10
    30
SerProValA laProAlaCy sAspProArg LeuLeuAsnL ysLeuLeuAr gAspSerHis LeuLeuHisS erArgLeuSe rGlnCysPro AspValAspPro
201 AGCCCCGTAG CTCTGCTCTG TGACCCCGA CTCTTAATAA AACTGCTCGG TGACTCCAC CTCTTTCACA GCGGACTCAG TCAGTGTCCC GAGCTCGACC
    40
LeuSerIl eProValLeu LeuProAlaV alAspPheSe rLeuGlyGlu TrpLysThrG lnThrGluGl nSerLysAla GlnAspIleL euGlyAlaVal
301 CTCTGTCTAT CCTGTGTTCTG CTGCTCTGCTG TGCACTTTAG CCTGGCAGAA TGGAAAGCC AGACCGAACA GAGCGAGCCA CAGGACATTC TAGGGCCAGT
    60
70
SerLeuLeu LeuGluGlyV alMetAlaAl aArgGlyGln LeuGluProS erCysLeuSe rSerLeuLeu GlyGlnLeuS erGlyGlnVa lArgLeuLeu
401 GTCCCTTCTA CTGAGGGGAG TGATGCCAGC ACCAGGACAG TTTGGAAACCCT CCTGCCCTCTC ATCCCTCTCTG CGACAGCTTT CTGGCCAGGT TCGCCTCTCTC
    80
    90
    100
LeuGlyAlaL euGlnGlyLe uLeuGlyThr GlnGlyArgf hrThrAlaHi sLysAspPro AsnAlaLeuP heLeuSerLe uGlnGlnLeu LeuArgGlyLys
501 TTGGGGGGCC TGCAGGGCCCT CCTAGCAACC CAGGGCAGGA CCACAGCTCA CAAGGACCCC AATGCCCTCT TCTTGAGCTT CCACCAACTG CTTGCGGGAA
    110
    120
    130
ValArgPh eLeuLeuLeu ValGluGlyP roThrLeuCy sValArgArg ThrLeuProT hrThrAlaVa lProSerSer ThrSerGlnL euLeuThrLeu
601 AGGTGCGCTT CTGCTTCTG GTAGAGGTC CCACCTCTG TGTCAGACGG ACCCTGCCAA CCACAGCTGT CCCAAGCAGT ACTTCTCAAC TCCTCAGACT
    140
    150
    160

```

FIG. 14B

```

170      180      190      200
AsnLysPhe ProAsnArgT hrSerGlyLe uLeuGluThr AsnPheSerV alThrAlaLea gThrAlaGly ProGlyLeuL euSerArgLe uGlnGlyPhe
701 AAACAAGTTC CCAACAGGA CTCTCGATT GTTCGAGAGG AACTTCAGTG TCACAGCCAG AACTGCTGC CTGCACTTC TCAGCAGCCT TCAGCGATTTC

      210      220      230
ArgValLysI leThrProG1 yGlnLeuAsn GlnThrSera rgSerProVa lGlnIleSer GlyDyTLeuA snArgThrHI sGlyProVal AsnGlyThrHis
801 AGAGTCAAGA TTACTCTCTG TCAGCTAAT CAACCTCCA GGTCCCCAGT CCAATCTCT CGATACCTCA ACAGGACACA CGACCTGTG AATGCAACTC

      240      250      260
GlyLeuPh eAlaGlyThr SerLeuGlnT hrLeuGluAl aSerAspIle SerProGlyA laPheAsnLy sGlySerLeu AlaPheAsnL euGlnGlyGly
901 ATGGGCTCTT TCCTGGAACC TCACCTTCAGA CCTGGGAAGC CTCAGACATC TCGCCCGGAG CTTTCAACAA AGGCTCCCTG GCATTCAACC TCACAGGGTGG

      270      280      290      300
LeuProPro SerProSerL euAlaProAs pGlyHisThr ProPheProp roSerProAl aleuProThr ThrHisGlys erProProGl nLeuHisPro
1001 ACTTCTCTCT TCTCCAAGCC TTGCTCTCTGA TGGACACACA CCGTTCCCTC CTTACACCTGC CTGCCCCACC ACCCATGGAT CTCACACCCA GCTCCACCCC

      310      320      330
LeuPheProA spProSerTh rThrMetPro AsnSerThra laProHisPr oValThrMet TyrProHisP roArganLe uSerGlnGlu Thr
1101 CTCTTTTCTG ACCCTTCCAC CACCATGGCT AACTCTACCG CCGCTCATCC AGTCACAATG TACCTTCATC CAGGAAATT GTCTCAGGAA ACATAGCGCG

      340      350      360
GGCACTGGCC CAGTCAGCCT CTGCAGCTTC TCTCGGGGAC AAGCTTCCCC AAGGCGAGCT GCATCTGCTC CAGATGTTCT GCTTTCACCT

      370      380      390
AAAGGCGCCT GGGGAGCGGA TACACAGCAC TCGAGATTGT AAAATTITAG GAGCTATTTT TTTTAACTT ATCAGCAATA TTCATCAGAG CAGCTAGCGA

      400
TCTTTGGTCT ATTTCGGTA TAAATTTCGA ATCACTAAT TCT

```

210 LeuGlnGlyPheArgValIysIleThrProGlyGlnLeuSngInrThrSerArgSerProValGlnIleSerGlyTyrLeuSngInrThrHisGlyProVal
 230 801 CTTCAGGATTGAGATCAAGATTACTCTGTCAGCTAAATCAAAACCTCCAGTCCCGACGCAAAATCTCTGGATACCTGAACAGGACACACGGACCTG
 240
 250
 260
 270
 280
 290
 300
 310
 320
 330
 340
 350
 360
 370
 380
 390
 400
 410
 420
 430
 440
 450
 460
 470
 480
 490
 500
 510
 520
 530
 540
 550
 560
 570
 580
 590
 600
 610
 620
 630
 640
 650
 660
 670
 680
 690
 700
 710
 720
 730
 740
 750
 760
 770
 780
 790
 800
 810
 820
 830
 840
 850
 860
 870
 880
 890
 900
 910
 920
 930
 940
 950
 960
 970
 980
 990
 1000
 1010
 1020
 1030
 1040
 1050
 1060
 1070
 1080
 1090
 1100
 1110
 1120
 1130
 1140
 1150
 1160
 1170
 1180
 1190
 1200
 1210
 1220
 1230
 1240
 1250
 1260
 1270
 1280
 1290
 1300
 1310
 1320
 1330
 1340
 1350
 1360
 1370
 1380
 1390
 1400
 1410
 1420
 1430
 1440
 1450
 1460
 1470
 1480
 1490
 1500
 1510
 1520
 1530
 1540
 1550
 1560
 1570
 1580
 1590
 1600
 1610
 1620
 1630
 1640
 1650
 1660
 1670
 1680
 1690
 1700
 1710
 1720
 1730
 1740
 1750
 1760
 1770
 1780
 1790
 1800
 1810
 1820
 1830
 1840
 1850
 1860
 1870
 1880
 1890
 1900
 1910
 1920
 1930
 1940
 1950
 1960
 1970
 1980
 1990
 2000
 2010
 2020
 2030
 2040
 2050
 2060
 2070
 2080
 2090
 2100
 2110
 2120
 2130
 2140
 2150
 2160
 2170
 2180
 2190
 2200
 2210
 2220
 2230
 2240
 2250
 2260
 2270
 2280
 2290
 2300
 2310
 2320
 2330
 2340
 2350
 2360
 2370
 2380
 2390
 2400
 2410
 2420
 2430
 2440
 2450
 2460
 2470
 2480
 2490
 2500
 2510
 2520
 2530
 2540
 2550
 2560
 2570
 2580
 2590
 2600
 2610
 2620
 2630
 2640
 2650
 2660
 2670
 2680
 2690
 2700
 2710
 2720
 2730
 2740
 2750
 2760
 2770
 2780
 2790
 2800
 2810
 2820
 2830
 2840
 2850
 2860
 2870
 2880
 2890
 2900
 2910
 2920
 2930
 2940
 2950
 2960
 2970
 2980
 2990
 3000
 3010
 3020
 3030
 3040
 3050
 3060
 3070
 3080
 3090
 3100
 3110
 3120
 3130
 3140
 3150
 3160
 3170
 3180
 3190
 3200
 3210
 3220
 3230
 3240
 3250
 3260
 3270
 3280
 3290
 3300
 3310
 3320
 3330
 3340
 3350
 3360
 3370
 3380
 3390
 3400
 3410
 3420
 3430
 3440
 3450
 3460
 3470
 3480
 3490
 3500
 3510
 3520
 3530
 3540
 3550
 3560
 3570
 3580
 3590
 3600
 3610
 3620
 3630
 3640
 3650
 3660
 3670
 3680
 3690
 3700
 3710
 3720
 3730
 3740
 3750
 3760
 3770
 3780
 3790
 3800
 3810
 3820
 3830
 3840
 3850
 3860
 3870
 3880
 3890
 3900
 3910
 3920
 3930
 3940
 3950
 3960
 3970
 3980
 3990
 4000
 4010
 4020
 4030
 4040
 4050
 4060
 4070
 4080
 4090
 4100
 4110
 4120
 4130
 4140
 4150
 4160
 4170
 4180
 4190
 4200
 4210
 4220
 4230
 4240
 4250
 4260
 4270
 4280
 4290
 4300
 4310
 4320
 4330
 4340
 4350
 4360
 4370
 4380
 4390
 4400
 4410
 4420
 4430
 4440
 4450
 4460
 4470
 4480
 4490
 4500
 4510
 4520
 4530
 4540
 4550
 4560
 4570
 4580
 4590
 4600
 4610
 4620
 4630
 4640
 4650
 4660
 4670
 4680
 4690
 4700
 4710
 4720

FIG. 15A

1 g a g t c c t t g g c c c a c c t c t c t c c c a c c c g a c t c t g c c g a a g a g c a c a g a g t c a a g c c g c c t c c a t g g c c c a g g a a g a t t c a g g g g a g a g g c c c c

MetGluLeuThrAspLeuLeuAlaAlaMetLeuLeuAlaValAlaArgLeuThrLeuSer
1101 a t a c a g g g a g c c a c t t c a g t t a g a c a c c c t g g c c a g a a i g g a g c t g a c t g a t t g c t c t g c g g c c a t g c t t c t t g c a g t g g c a a g a c t a a c t c t g t c c

20 30
SerProValAlaProAlaCysAspProArgLeuLeuAsnLysLeuLeuArgAspSerHisLeuLeuHisSerArgLeuSerGlnCysProAspValAspPro
2201 a g c c c c t a g c t c c t g t g a c c c c a g a c t c c t a a t a a c t g c t g c g t g a c t c c c a c c t c c t t t c a c a g c c a c t g a g t c a g t g t c c c g a c g t c g a c c

40 50 60
LeuSerIleProValLeuLeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnThrGluGlnSerLysAlaGlnAspIleLeuGlyAlaVal
3301 c t t t g t c t a t c c c t g t t c t g c t g c c t g c t g t g a c t t t a g c c t g g a g a a t g g a a a a c c c a g a c g g a c a g a g c a c a g g a c a t t c t a g g g g c a g t

80 90 100
SerLeuLeuLeuGluGlyValMetAlaAlaArgGlyGlnLeuGluProSerCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeu
401 g t c c c t t c t a c t g g a g g g a g t g a t g c c a g c a c g a g a c a g t t g g a a c c c t c c t g c t c t a t c c c t c c t g g a c a c a g c t t t t c t g g c a g g t t c g c c t c c t c

110 120 130
LeuGlyAlaLeuGlnGlyLeuLeuGlyThrGlnLeuProLeuGlnGlyArgThrAlaAlaHisLysAspProAsnAlaLeuPheLeuSerLeuGlnGlnLeu
501 t t g g g g c c c t g c a g g c c t c c t a g g a a c c c a g c t c c t c t a c a g g c c a g g a c a g c t c a c a a g g a c c c a a t g c c c t c t t c t t g a g c t t t g c a a c a a c

140 150 160
LeuArgGlyLysValArgPheLeuLeuLeuValGluGlyProThrLeuCysValArgArgThrLeuProThrThrAlaValProSerSerThrSerGln
601 t g c t t c g g g a a a g g t g c g c t t c c t g c t t c t g g t a g a a g g t c c c a c c c t g t g t a g a c g a c c c t g c c a c c a c a g c t g t c c c a a g c a g t a c t c t c a

170 180 190 200
LeuLeuThrLeuAsnLysPheProAsnAlaThrSerGlyLeuLeuGluThrAspPheSerValThrAlaArgThrAlaGlyProGlyLeuLeuSerArg
701 a c t c c t c a c a c t a a c a a g t c c c a a c a g g a c t t c t g g a t t g t t g g a g a c a a c a c a g a t c a g c c a g a c a g c c t g c c c t g g a c t t c t a g a c a g g

FIG. 15B

[illegible]

FIG. 16

hML3 1 SPAPACDILRVLSKLLRDSHVLSHSRLSQCPVHPLPTIPVLLPAVDFSLGE
mML3 1 SPVAPACDPRLLNKLLRDSHLLHSRLSQCPVDPLSIPVLLPAVDFSLGE

hML3 51 WKTOMETKAODILGAVTLLLEGVMAARGQLGPTCLSSLLGQLSGQVRLL
mML3 51 WKTOETEKSKAODILGAVSLLLEGVMAARGOLEPSCLSSLLGQLSGQVRLL

hML3 101 LGALQSLLGTQLPPQGRITTAHKDPNAIFLSFQHLRLRGKDFWIVGDKLHCL
mML3 101 LGALQGLLGTQLPLQGRITTAHKDPNALFLSLQQLRLRGKDFWIVGDELOCH

hML3 151 SONYWLWASEVAAGIQSQD-SWSAEPNLQVPGPNPIPEQDTRTLEWNSW
mML3 151 SONCWPTWTSSEQASGIQSQDYSWSAKSNLQVPSPNLWIPEDQDTRTCEWNSW

hML3 200 TLSWTLTQDPRS PGHFLRNIRHRLPATQPPAWIFSFPNPSYWTXYALPS
mML3 201 ALCWNLTSQDPSLRHLARSFQORLPGIQPPGWTSFSKPCCS

hML3 250 STHLAHPCGPAPPAS

FIG. 17

FIG.17A

m-ML	1	S	P	V	A	P	A	C	D	P	R	L	N	K	L	R	D	S	H	L	L	H	S	R	L	S	O	C	P	D	V	D	P	L	S	I	P	V	L	L	P	A	V	D	F	S	L	G	E		
p-ML	1	S	P	A	P	P	A	C	D	P	R	L	N	K	L	R	D	S	H	V	L	H	G	R	L	S	O	C	P	D	I	N	P	L	S	T	P	V	L	L	P	A	V	D	F	T	L	G	E		
h-ML	1	S	P	A	P	A	C	D	L	R	V	L	S	K	L	R	D	S	H	V	L	H	S	R	L	S	O	C	P	E	V	H	P	L	P	T	P	V	L	L	P	A	V	D	F	S	L	G	E		
m-ML	51	W	K	T	Q	T	E	O	S	K	A	Q	D	I	L	G	A	V	S	L	L	L	E	G	V	M	A	A	R	G	O	L	E	P	S	C	L	S	S	L	L	G	O	L	S	G	O	V	R	L	L
p-ML	51	W	K	T	Q	T	E	Q	T	K	A	Q	D	V	L	G	A	T	T	L	L	E	A	V	M	T	A	R	G	O	V	G	P	P	C	L	S	S	L	L	V	Q	L	S	G	O	V	R	L	L	
h-ML	51	W	K	T	O	M	E	T	K	A	Q	D	I	L	G	A	V	T	L	L	L	E	G	V	M	A	A	R	G	O	L	G	P	T	C	L	S	S	L	L	G	O	L	S	G	O	V	R	L	L	
m-ML	101	L	G	A	L	Q	G	L	L	G	T	Q	L	P	L	Q	G	R	T	T	A	H	K	D	P	N	A	L	F	L	S	L	Q	Q	L	L	R	G	K	V	R	F	L	L	V	E	G	P	T	L	
p-ML	101	L	G	A	L	Q	D	L	L	G	M	Q	L	P	P	Q	G	R	T	T	A	H	K	D	P	S	A	I	F	L	N	F	O	Q	L	L	R	G	K	V	R	F	L	L	V	V	G	P	S	L	
h-ML	101	L	G	A	L	Q	S	L	L	G	T	Q	L	P	P	Q	G	R	T	T	A	H	K	D	P	N	A	I	F	L	S	F	O	H	L	L	R	G	K	V	R	F	L	M	L	V	G	S	T	L	

FIG.17B

m-ML	151	C	V	R	R	T	L	P	T	T	A	V	P	S	S	T	S	Q	L	L	T	L	N	K	F	P	N	R	T	S	G	L	L	E	T	N	F	S	V	T	A	R	T	A	G	P	G	L	L	S	R
p-ML	151	C	A	K	R	A	P	P	A	I	A	V	P	S	S	T	S	P	F	H	T	L	N	K	L	P	N	R	T	S	G	L	L	E	T	N	S	S	I	S	A	R	T	T	G	S	G	F	L	K	R
h-ML	151	C	V	R	R	A	P	P	T	T	A	V	P	S	R	T	S	L	V	L	T	L	N	E	L	P	N	R	T	S	G	L	L	E	T	N	F	I	A	S	A	R	T	T	G	S	G	L	L	K	W
m-ML	201	L	Q	G	F	R	V	K	I	T	P	G	Q	L	N	O	T	S	R	S	P	V	Q	I	S	G	Y	L	N	R	T	H	G	P	V	N	G	I	H	G	L	F	A	G	T	S	L	O	T	L	E
p-ML	201	L	Q	A	F	R	A	K	I	-	P	G	L	L	N	O	T	S	R	S	L	D	Q	I	P	G	H	Q	N	G	I	H	G	P	L	S	G	I	H	G	L	F	P	G	P	Q	P	G	A	L	G
h-ML	201	Q	Q	G	F	R	A	K	I	-	P	G	L	L	N	O	T	S	R	S	L	D	Q	I	P	G	Y	L	N	R	I	H	E	L	L	N	G	T	R	G	L	F	P	G	P	S	R	R	T	L	G
m-ML	251	A	S	D	I	S	P	G	A	F	N	K	G	S	L	A	F	N	L	Q	G	L	P	P	S	P	S	L	A	P	D	G	H	-	T	P	F	P	P	S	P	A	L	P	T	H	G	S	P		
p-ML	250	A	P	D	I	P	A	T	S	G	M	G	S	R	P	T	Y	L	Q	P	G	E	S	P	S	P	A	H	P	S	P	G	R	Y	T	L	F	S	P	S	P	T	S	P	S	-	-	P	T		
h-ML	250	A	P	D	I	S	S	G	T	S	D	T	G	S	L	P	P	N	L	Q	P	G	Y	S	P	S	P	T	H	P	P	T	G	Q	Y	T	L	F	P	L	P	T	L	P	T	-	-	P	V		
m-ML	300	P	Q	L	H	P	L	F	P	D	P	S	T	T	M	P	N	S	T	A	P	H	P	V	T	M	Y	P	H	P	R	N	E	L	S	Q	E	T													
p-ML	297	V	Q	L	Q	P	L	L	P	D	P	S	A	I	T	P	N	S	T	S	P	L	L	F	A	A	H	P	H	F	Q	N	L	S	Q	E	E														
h-ML	297	V	Q	L	H	P	L	L	P	D	P	S	A	P	T	P	T	S	P	L	L	N	T	S	Y	T	H	S	Q	N	L	S	Q	E	G																

FIG. 17A

m-ML	1	S	P	V	A	P	A	C	D	P	R	L	N	K	L	R	D	S	H	L	H	S	R	L	S	Q	C	P	D	V	D	P	L	S	I	P	V	L	L	P	A	V	D	F	S	L	G	E			
p-ML	1	S	P	A	P	P	A	C	D	P	R	L	N	K	L	R	D	S	H	V	L	H	G	R	L	S	Q	C	P	D	I	N	P	L	S	T	P	V	L	L	P	A	V	D	F	T	L	G	E		
h-ML	1	S	P	A	P	P	A	C	D	L	R	V	L	S	K	L	R	D	S	H	V	L	H	S	R	L	S	Q	C	P	E	V	H	P	L	P	T	P	V	L	L	P	A	V	D	F	S	L	G	E	
m-ML	51	W	K	T	Q	T	E	Q	S	K	A	Q	D	I	L	G	A	V	S	L	L	L	E	G	V	M	A	A	R	G	Q	L	E	P	S	C	L	S	S	L	L	G	Q	L	S	G	Q	V	R	L	L
p-ML	51	W	K	T	Q	T	E	Q	T	K	A	Q	D	V	L	G	A	T	T	L	L	L	E	A	V	M	T	A	R	G	Q	V	G	P	P	C	L	S	S	L	L	V	Q	L	S	G	Q	V	R	L	L
h-ML	51	W	K	T	Q	M	E	E	T	K	A	Q	D	I	L	G	A	V	T	L	L	L	E	G	V	M	A	A	R	G	Q	L	G	P	T	C	L	S	S	L	L	G	Q	L	S	G	Q	V	R	L	L
m-ML	101	L	G	A	L	Q	G	L	L	G	T	Q	L	P	L	Q	G	R	T	T	A	H	K	D	P	N	A	L	F	L	S	L	Q	Q	L	L	R	G	K	V	R	F	L	L	V	E	G	P	T	L	
p-ML	101	L	G	A	L	Q	D	L	L	G	M	Q	L	P	P	Q	G	R	T	T	A	H	K	D	P	P	S	A	I	F	L	N	F	Q	Q	L	L	R	G	K	V	R	F	L	L	V	V	G	P	S	L
h-ML	101	L	G	A	L	Q	S	L	L	G	T	Q	L	P	P	Q	G	R	T	T	A	H	K	D	P	N	A	I	F	L	S	F	Q	H	L	L	R	G	K	V	R	F	L	M	L	V	G	S	T	L	

FIG.17B

m-ML	151	C	V	R	R	T	L	P	T	T	A	V	P	S	S	T	S	Q	L	T	L	N	K	F	P	N	R	T	S	G	L	L	E	T	N	F	S	V	T	A	R	T	A	G	P	G	L	L	S	R				
p-ML	151	C	A	K	R	A	P	P	A	I	A	V	P	S	S	T	S	P	F	H	T	L	N	K	L	P	N	R	T	S	G	L	L	E	T	N	S	I	S	A	R	T	T	G	S	G	F	L	K	R				
h-ML	151	C	V	R	R	A	P	P	T	T	A	V	P	S	R	T	S	L	V	L	T	L	N	E	L	P	N	R	T	S	G	L	L	E	T	N	F	T	A	S	A	R	T	T	G	S	G	L	L	K	W			
m-ML	201	L	O	G	F	R	V	K	I	T	P	G	Q	L	N	Q	T	S	R	S	P	V	Q	I	S	G	Y	L	N	R	T	H	G	P	V	N	G	T	H	G	L	F	A	G	T	S	L	Q	T	L	E			
p-ML	201	L	Q	A	F	R	A	K	I	-	P	G	L	L	N	Q	T	S	R	S	L	D	Q	I	P	G	H	Q	N	G	T	H	G	P	L	S	G	I	H	G	L	F	P	G	P	Q	P	G	A	L	G			
h-ML	201	Q	Q	G	F	R	A	K	I	-	P	G	L	L	N	Q	T	S	R	S	L	D	Q	I	P	G	Y	L	N	R	I	H	E	L	L	N	G	T	R	G	L	F	P	G	P	S	R	R	T	L	G			
m-ML	251	A	S	D	I	S	P	G	A	F	N	K	G	S	L	A	F	N	L	Q	G	G	L	P	P	S	P	S	L	A	P	D	G	H	-	T	P	F	P	P	S	P	A	L	P	T	T	H	G	S	P			
p-ML	250	A	P	D	I	P	A	T	S	G	M	G	S	R	P	T	Y	L	Q	P	G	E	S	P	S	P	A	H	P	S	P	A	H	P	S	P	G	R	Y	T	L	F	S	P	S	P	T	S	P	S	-	-	P	T
h-ML	250	A	P	D	I	S	G	T	S	D	T	G	S	L	P	P	N	L	Q	P	G	Y	S	P	S	P	T	H	P	P	T	G	Q	Y	T	L	F	P	L	P	P	T	L	P	T	-	-	-	P	V				
m-ML	300	P	Q	L	H	P	L	F	P	D	P	S	T	T	M	P	N	S	T	A	P	H	P	V	T	M	Y	P	H	P	R	N	L	S	Q	E	T																	
p-ML	297	V	Q	L	Q	P	L	L	P	D	P	S	A	I	T	P	N	S	T	S	P	L	L	F	A	A	H	P	H	F	Q	N	L	S	Q	E	E																	
h-ML	297	V	Q	L	H	P	L	L	P	D	P	S	A	P	T	P	T	S	P	L	L	N	T	S	Y	T	H	S	Q	N	L	S	Q	E	G																			

FIG. 18B

8B

LeuGlnAlaPheArgAlaLysIleProGlyLeuLeuAsnGlnThrSerArgSerLeuAspGlnIleProGlyHisGlnAsnGlyThrHisGlyProLeuSer
601 CTGCAGGCATTACAGGCCAAGATTCTTGTTCTGTGAACCAAACTCCAGGTCCTTAGACCATAATCCTCGACACACCGAACCTTGA

GlyIleHisGlyLeuPheProGlyProGlnProGlyAlaLeuGlyAlaProAspIleProProAlaThrSerGlyMetGlySerArgProThrTyrLeu
701 GTGGAAATCATGGACTCTTTCTCGGACCCCAACCCGGGGCCCTCGGAGCTCCAGACATTCTCCAGCAACTTCAGGCATGGGCTCCCCGGCCAACCTACCT

GlnProGlyGluSerProSerProAlaHisProSerProGlyArgTyrThrLeuPheSerProSerProThrSerProSerProThrValGlnLeuGln
801 CCAGCCTGGAGAGTCCTCTTCCCAGCTCACCCCTTCTCTCTGGACGATACACTCTCTCTCTCTCTCCTTCAACCACCTCGCCCTCCCCACAGTCCAGCTCCAG

ProLeuLeuProAspProSerAlaIleThrProAsnSerThrSerProLeuLeuPheAlaAlaHisProHisPheGlnAsnLeuSerGlnGluGlu
901 CCTCTGTCTCTGACCCCTCTCGGATCACAACCCAACTCTACCAGTCCTCTTCTATTGTCAGCTCACCCCTCATTTCCAGAACCTGTCTCAGGAAGAGTAAG

1001 GTGCTCAGACCCCTGCCAACTTCAGCA

FIG.18A

	10	20	30
SerProAlaProProAlaCysAspProArgLeuLeuAsnLysLeuLeuArgAspSerHisValLeuHisGlyArgLeuSerGlnCysProAspIleAsnPro			
1 AGCCCGGCTCCTTCCTGCTGTGACCCCGACTCCTCTAAATAAACTGCTTCGTGACTCCCATGTCCTTCACGGCAGACTGAGCCAGTGCCCGACACATTAAACC			
	40	50	60
LeuSerThrProValLeuLeuProAlaValAspPheThrLeuGlyGluTrpLysThrGlnThrGluGlnThrLysAlaGlnAspValLeuGlyAlaThr			
101 CTTTGTCCACACCTGTCTCCTGCTGTGACCTTCACCTTGGGAGAAATGGAAACCCAGACGGAGCAGACAAAGGCACAGGATGTCTCTGGGAGCCAC			
	70	80	90
ThrLeuLeuLeuGluAlaValMetThrAlaArgGlyGlnValGlyProProCysLeuSerSerLeuLeuValGlnLeuSerGlyGlnValArgLeuLeu			
201 AACCTTCTGCTGGAGGCCAGTGATGACAGCACGGGGACAAAGTGGGACCCCTTGCTCTCATCCCTGCTGGTGCAGCTTCTCGGACAGGTTCCGCTCCCTC			
	110	120	130
LeuGlyAlaLeuGlnAspLeuLeuGlyMetGlnLeuProProGlnGlyArgThrThrAlaHisLysAspProSerAlaIlePheLeuAsnPheGlnGlnLeu			
301 CTCGGGGCCCTGCAGGACCTCCTTGGAAATGCAGCTTCCTCCACAGGGAAGGACCACAGCTCACAGGATCCCGAGTGCCCATCTTCTGAACTTCCAACAAC			
	140	150	160
LeuArgGlyLysValArgPheLeuLeuLeuValValGlyProSerLeuCysAlaLysArgAlaProProAlaIleAlaValProSerSerThrSerPro			
401 TGCTCCGAGGAAAGGTGCGTTTCTGCTCCTTGTAGTGGGGCCCTCCCTCTGTGCCAAGAGGGCCCCACCCGCCCATAGCTGTCTCCCGAGCAGCACCTCTCTCC			
	170	180	190
PheHisThrLeuAsnLysLeuProAsnArgThrSerGlyLeuLeuGluThrAsnSerSerIleSerAlaArgThrThrGlySerGlyPheLeuLysArg			
501 ATTCCACACACTGAACAAGCTCCCAACACAGGACCTCTGGATTGTTGGAGACAAACTCCAGTATCTCAGCCAGAACTACTGGCTCTGGATTCTCAAGAGG			

210 LeuGlnAlaPheArgAlaIleProGlyLeuLeuAsnGlnThrSerArgSerLeuAspGlnIleProGlyHisGlnAsnGlyThrHisGlyProLeuSer
 230
 601 CTGCAGGCATTCAGACCAAGATTCCCTGGTCTGCTGAACCAAAACCTCCAGGTCCCTAGACCAAAATCCCTGGACACACAGATGGACACACGGACCCCTTGA
 240
 GlyIleHisGlyLeuPheProGlyProGlnProGlyAlaLeuGlyAlaProAspIleProProAlaThrSerGlyMetGlySerArgProThrTyrLeu
 260
 701 GTGGAATTTCATGGACTCTTTCTCGGACCCCAACCCGGGCCCTCGGAGCTCCAGACATTCTCCAGCAACTTCAGGCATGGGCTCCCGGCCCAACCTTACCT
 280
 GlnProGlyGluSerProSerProAlaHisProSerProGlyArgTyrThrLeuPheSerProSerProThrSerProSerProThrValGlnLeuGln
 300
 801 CCAGCCTGGAGAGTCTCCTTCCCCAGCTCACCTTCTCCCTGGACGATACACTCTCTCTCTCTCCCTTACCCCACTCGCCCTCCCCACAGTCCAGCTCCAG
 310
 ProLeuLeuProAspProSerAlaIleThrProAsnSerThrSerProLeuLeuPheAlaAlaHisProHisPheGlnAsnLeuSerGlnGluGlu
 330
 901 CCTCTGCTTCCCTGACCCCTCTGCGGATCACACCCAACTCTACCAAGTCTCTTCTATTTGCAGTCAACCTTCAGAACTGTCTCAGGAAGAGTAAG
 1001 GTGCTCAGACCCCTGCCAACTTCAGCA

FIG. 19B

170 AsnLysLeuProAsnArgThrSerGlyLeuLeuGluThrAsnSerIleSerAlaArgThrThrGlySerGlyPheLeuLysArgLeuGlnAlaPhe 190 200
501 GAACAAGCTCCCAACAGGACCTCTGGATTGTGTGGAGACAAACTCCAGTATCTCAGCCAGAACTACTGGCTCTGGATTTCTCAAGAGGCTGCAGGCATTC 230
210 220 230
601 ArgAlaLysIleProGlyLeuLeuAsnGlnThrSerArgSerLeuAspGlnIleProGlyHisGlnAsnGlyThrHisGlyProLeuSerGlyIleHisGly 260
AGAGCCAAAGATTCTCTGGTGTGTAACCAACCTCCAGGTCCCTAGACCAATAATCCCTGGACACACAGAAATGGGACACACGGACCCCTTGAGTGGGAATTCATG 260
240 250 260
LeuPheProGlyProGlnProGlyAlaLeuGlyAlaProAspIleProProAlaThrSerGlyMetGlySerArgProThrTyrLeuGlnProGlyGlu 270 300
701 GACTCTTTCTGGACCCCAACCCGGGGCCCTCGAGCTCCAGACATTCCTCCAGCAACTTCAGGCATGGGCTCCCGGCCAACCTACCTCCAGCCTGGAGA 300
270 280 290 300
SerProSerProAlaHisProSerProGlyArgTyrThrLeuPheSerProSerProThrSerProSerProThrValGlnLeuGlnProLeuLeuPro 310 320
801 GTCTCTTTCCCAAGCTCACCCCTTCCTCTGGACGATACACTCTCTTCTCTCTTCACCCACCTCGCCCTCCCCACAGTCCAGCTCCAGCCTCTGCTTCCT 320
310 320
AspProSerAlaIleThrProAsnSerThrSerProLeuLeuPheAlaAlaHisProHisPheGlnAsnLeuSerGlnGlu 330
901 GACCCCTCTGGGATCACACCCAACTCTACCAGTCTCTTCTATTGTGAGCTCACCCCTCAATTTCAGAAACCTGTCTCAGGAAGAGTAAGGTGCTCAGACCC 330
1001 TGCCCAACTTCAGCA

FIG. 19A

	10	20	30
SerProAlaProProAlaCysAspProArgLeuLeuAsnLysLeuLeuArgAspSerHisValLeuHisGlyArgLeuSerGlnCysProAspIleAsnPro			
1	AGCCCGGCTCCTCCTGCTGTGACCTCCTAAATAAACTGCTTCGTGACTCCCATGCTCCTTCACGGCAGACTGAGCCAGTGCACATTAACC		
	40	50	60
LeuSerThrProValLeuLeuProAlaValAspPheThrLeuGlyGluTrpLysThrGlnThrGluGlnThrLysAlaGlnAspValLeuGlyAlaThr			
101	CTTTGTCCACACCTGTCTGCTGCTGCTGTGACTTCACTTGGGAGAAATGGAAACCCAGACGGAGCAGACAAAGGCACAGGATGTCCTGGGAGCCAC		
	70	80	90
ThrLeuLeuLeuGluAlaValMetThrAlaArgGlyGlnValGlyProProCysLeuSerSerLeuLeuValGlnLeuSerGlyGlnValArgLeuLeu			
201	AACCCCTTCTGCTGGAGGCAGTGATGACAGCACGGGGACAAGTGGGACCCCTTGCCCTCTCATCCCTGCTGGTGCAGCTTTCCTGGACAGGTTCCGCTCCTC		
	110	120	130
LeuGlyAlaLeuGlnAspLeuLeuGlyMetGlnGlyArgThrThrAlaHisLysAspProSerAlaIlePheLeuAsnPheGlnGlnLeuLeuArgGlyLys			
301	CTCGGGGCCCCGACGACCTCCTTGGAAATGCAGGGAAGGACCACAGCTCACAGGATCCCAGTGCCCATCTTCTGAACTTCCAACTGCTCCGAGGAA		
	140	150	160
ValArgPheLeuLeuLeuValValGlyProSerLeuCysAlaLysArgAlaProProAlaIleAlaValProSerSerThrSerProPheHisThrLeu			
401	AGGTGCGTTTCTCCTGCTTGTAGTGGGGCCCTCCCTCTGTGCCAAGAGGGCCCCACCCGCCCATAGCTGTCCCGAGCAGCACCTCTCCATTCCACACACT		

FIG. 19B

```

170                                     180                                     190                                     200
AsnLysLeuProAsnArgThrSerGlyLeuLeuGluThrAsnSerSerIleSerAlaArgThrThrGlySerGlyPheLeuLysArgLeuGlnAlaPhe
501 GAACAAGCTCCCAACAGGACCTCTGGATTGTTGGAGACAAACTCCAGTATCTCAGCCAGAACTACTGGCTCTGGATTCTCAAGAGGCTGCAGGCATTCTC
                                     210                                     220                                     230
ArgAlaLysIleProGlyLeuLeuAsnGlnThrSerArgSerLeuAspGlnIleProGlyHisGlnAsnGlyThrHisGlyProLeuSerGlyIleHisGly
601 AGAGCCAAAGATTCTGGTCTGCTGAACCAACCTCCAGGTCCCTAGACCAAAATCCCTGGACACCCAGAAATGGGACACACACGGACCCCTTGAGTGGAAATTTCATG
                                     240                                     250                                     260
LeuPheProGlyProGlnProGlyAlaLeuGlyAlaProAspIleProProAlaThrSerGlyMetGlySerArgProThrTyrLeuGlnProGlyGlu
701 GACTCTTTCTGGACCCCAACCCGGGGCCCTCGGAGCTCCAGACATTCTCTCCAGCAACTTCAGGCATGGGCTCCCGGCCAACCTACCTCCAGCCTGGAGA
                                     270                                     280                                     290                                     300
SerProSerProAlaHisProSerProGlyArgTyrThrLeuPheSerProSerProThrSerProSerProThrValGlnLeuGlnProLeuLeuPro
801 GTCTCCTTCCCCAGCTCACCTTCTCCTGGACGATACACTCTCTTCTCTCTCCTTACCCACCTCGCCCTCCCCACAGTCCAGCTCCAGCCTCTGCTTCCT
                                     310                                     320
AspProSerAlaIleThrProAsnSerThrSerProLeuLeuPheAlaAlaHisProHisPheGlnAsnLeuSerGlnGluGlu
901 GACCCCTCTGCGGATCACACCCCAACTCTACCAAGTCCCTCTTCTATTGTCAGCTCACCCCTCATTTTCCAGAACCTGTCTCAGGAAGAGTAAGGTGCTCAGACCC
1001 TGCCAACTTCAGCA

```

FIG. 20

FIG.20A

pML	1	SPAPPACOPRLLNKLLRDSHVLHGRLSQCPDINPLSTPVL LPAVDFTLGE
pML2	1	SPAPPACOPRLLNKLLRDSHVLHGRLSQCPDINPLSTPVL LPAVDFTLGE
pML	51	WKTEOTEOTKAODVLGATTL LLEAVMTARGOVGPPCLSSLLVQLSGOVRLL
pML2	51	WKTEOTEOTKAODVLGATTL LLEAVMTARGOVGPPCLSSLLVQLSGOVRLL
pML	101	LGALQD L L LGMOLPP
pML2	101	LGALQD L L LGM . . .

FIG.20B

pML	151	CAKRAPPAIAVPSSSTSPFH TLNKL PNR TSGLLE TNSSISARTTGS GFLKR
pML2	147	CAKRAPPAIAVPSSSTSPFH TLNKL PNR TSGLLE TNSSISARTTGS GFLKR
pML	201	LQAFRAKIPG L L N O T S R S L D Q I P G H O N G T H G P L S G I H G L F P G P Q P G A L G A
pML2	197	LQAFRAKIPG L L N O T S R S L D Q I P G H O N G T H G P L S G I H G L F P G P Q P G A L G A
pML	251	PDI'PPATSGMGSRPTYL OPGESPSPAHPSPGRYTL FSPSPTSPSPTVQLQ
pML2	247	PDI'PPATSGMGSRPTYL OPGESPSPAHPSPGRYTL FSPSPTSPSPTVQLQ
pML	301	PLLPDPSA ITPNSTSP L LFAAHPHFONLSQEE
pML2	297	PLLPDPSA ITPNSTSP L LFAAHPHFONLSQEE

FIG. 20A

pML	1	SPAPPACDPRLLNKLLRDSHVLHGRLSQCPDINPLSTPVL LPAVDFTLGE
pML2	1	SPAPPACDPRLLNKLLRDSHVLHGRLSQCPDINPLSTPVL LPAVDFTLGE
pML	51	WKTQTEOTKAODVLGATTLLLEAVMTARGOVGPPCLSSLLVQLSGOVRLL
pML2	51	WKTQTEOTKAODVLGATTLLLEAVMTARGOVGPPCLSSLLVQLSGOVRLL
pML	101	L GALQD L L G M O L P P O G R T T A H K D P S A I F L N F O Q L L R G K V R F L L L V V G P S L
pML2	101	L GALQD L L G M O G R T T A H K D P S A I F L N F O Q L L R G K V R F L L L V V G P S L

FIG. 20B

pML	151	CAKRAPPAAIAVPSSSTSPFFHTLNKLPNRTSGLLETNSSISARTTGS	GFLKR
pML2	167	CAKRAPPAAIAVPSSSTSPFFHTLNKLPNRTSGLLETNSSISARTTGS	GFLKR
pML	201	LOAFRAKIPGLLNQTSRSLDQIPGHONGTHGPLSGIHGLFPGPQ	P ¹ PGALGA
pML2	197	LOAFRAKIPGLLNQTSRSLDQIPGHONGTHGPLSGIHGLFPGPQ	P ¹ PGALGA
pML	251	PDIP ¹ PATSGMGSRPTYLQPGESPSPAHPSPGRYTLFSPSPT	SPSTVQLO
pML2	247	PDIP ¹ PATSGMGSRPTYLQPGESPSPAHPSPGRYTLFSPSPT	SPSTVQLO
pML	301	PLLP ¹ OPSAITPNSTSPILLFAAHPHFQNL	SOEE
pML2	297	PLLP ¹ OPSAITPNSTSPILLFAAHPHFQNL	SOEE